

WEST Search History

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DATE: Tuesday, April 13, 2004

Hide?	<u>Set Name</u>	<u>Query</u>	<u>Hit Count</u>
	<i>DB=PGPB,USPT,USOC,EPAB,JPAB,DWPI,TDBD; PLUR=YES; OP=AND</i>		
<input type="checkbox"/>	L1	ure near10 i	129479
<input type="checkbox"/>	L2	L1 and helicobacter	7
<input type="checkbox"/>	L3	urei.clm. or ure-i.clm.	36
<input type="checkbox"/>	L4	L3 not l2	34
<input type="checkbox"/>	L5	aime	4109
<input type="checkbox"/>	L6	L5 and helicobacter	2
<input type="checkbox"/>	L7	('6248551' '20030180330')!.PN.	4
<input type="checkbox"/>	L8	aliphatic near5 amidase	34
<input type="checkbox"/>	L9	L8 and (pylori or helicobacter or pyloris or pylroi or pyloridis or pylorum or hpylori or h-pylori)	9

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DATE: Tuesday, April 13, 2004

Hide?	Set Name	Query	Hit Count
		<i>DB=PGPB,USPT,USOC,EPAB,JPAB,DWPI,TDBD; PLUR=YES; OP=AND</i>	
<input type="checkbox"/>	L1	ure near10 i	129479
<input type="checkbox"/>	L2	L1 and helicobacter	7
<input type="checkbox"/>	L3	urei.clm. or ure-i.clm.	36
<input type="checkbox"/>	L4	L3 not l2	34
<input type="checkbox"/>	L5	aime	4109
<input type="checkbox"/>	L6	L5 and helicobacter	2
<input type="checkbox"/>	L7	('6248551' '20030180330')!.PN.	4

END OF SEARCH HISTORY

First Hit

☐ **Generate Collection** **Print**

L9: Entry 1 of 9

File: PGPB

Feb 19, 2004

DOCUMENT-IDENTIFIER: US 20040033549 A1

TITLE: Quorum sensing signaling in bacteria

Detail Description Paragraph:

[0088] The term "biofilm-associated disease or disorder" includes diseases, disorders or conditions which are characterized or caused by the presence or potential presence of a biofilm, e.g., a bacterial biofilm. Biofilm-associated diseases or disorders include infection of the subject by one or more bacteria, e.g., *Pseudomonas aeruginosa*, *Bacillus subtilis*, *Candida albicans*, *Staphylococcus aureus*, *Staphylococcus epidermidis*, *Enterococcus faecalis*, *Helicobacter pylori*, *Escherichia coli*, *Salmonella typhimurium*, *Legionella pneumophila*, or other gram-negative or gram positive bacteria. Examples of biofilm-associated diseases or disorders include diseases or disorders caused by, for example, bacteria (e.g., gram-positive and/or gram-negative bacteria), fungi, viruses and parasites. Examples of biofilm-associated diseases or disorders include, but are not limited to, cystic fibrosis, AIDS, middle ear infections, osteomyelitis, acne, dental cavities, prostatitis, abscesses, bacteremia, contamination of peritoneal dialysis fluid, endocarditis, pneumonia, meningitis, cellulitis, pharyngitis, otitis media, sinusitis, scarlet fever, arthritis, urinary tract infection, laryngotracheitis, erysipeloid, gas gangrene, tetanus, typhoid fever, acute gastroenteritis, bronchitis, epiglottitis, plague, sepsis, chancroid, wound and bum infection, cholera, glanders, periodontitis, genital infections, empyema, granuloma inguinale, Legionnaire's disease, paratyphoid, bacillary dysentery, brucellosis, diphtheria, pertussis, botulism, toxic shock syndrome, mastitis, rheumatic fever, eye infections, including contact lens infections, periodontal infections, catheter- or medical device-associated infections, and plaque. Other biofilm-associated diseases or disorders include swine erysipelas, peritonitis, abortion, encephalitis, anthrax, nocardiosis, pericarditis, mycetoma, peptic ulcer, melioidosis, Haverhill fever, tularemia, Moko disease, galls (such as crown, cane and leaf), hairy root, bacterial rot, bacterial blight, bacterial brown spot, bacterial wilt, bacterial fin rot, dropsy, columnaris disease, pasteurellosis, furunculosis, enteric redmouth disease, vibriosis of fish, and fouling of medical devices.

Detail Description Table CWU:

6TABLE 6 Quorum-repressed genes..sup.1 Maximum repression (fold).sup.c lasI.sup.- rhII.sup.- mutant Wt vs. Gene no..sup.a Description.sup.b 3OC12-HSL C4 + 3OC12-HSL lasR.sup.- rhIR.sup.- PA0165 hypothetical protein -2.7 -2.9 (2.0) -4.8 (2.0) PA0433 hypothetical protein -6.8 -19.7 (2.0) -8.9 (1.4) PA0434 hypothetical protein -7.7 -8.5 (2.0) -5.6 (2.0) PA0435 hypothetical protein -9.4 -25.5 (2.0) -33.8 (2.0) PA0485 conserved hypothetical protein.sup.c -1.7 -3.4 (1.4) -3.0 (3.0) PA0887 acsA, acetyl-coenzyme A synthetase -3.3 -4.2 (2.0) -3.6 (3.0) PA1559 hypothetical protein -2.4 -3.5 (2.0) -3.2 (1.4) PA2007 maiA, maleylacetoacetate isomerase -3.2 -1.4 (4.0) -3.2 (3.0) PA2008 fahA, fumarylacetoacetase -3.7 -1.5 (4.0) -2.6 (3.0) PA2009 hmgA, homogentisate 1,2-dioxygenase -4.0 -1.5 (4.0) -2.7 (3.0) PA2250 lpdV, lipoamide dehydrogenase-Val -3.1 -1.8 (4.0) -2.6 (3.0) PA2338 probable component of ABC maltose transporter -5.0 -3.2 (3.0) -4.2 (3.0) PA2339 probable maltose/mannitol transport protein -1.9 -6.8 (3.0) -4.1 (3.0) PA2340 probable maltose/mannitol transport protein -3.4 -2.0 (3.0) -3.7 (3.0) PA2341 probable component of ABC maltose transporter -3.1 -2.0 (3.0) -4.2 (3.0) PA2343 mtly, xylulose kinase -1.7 -

-4.0 (3.0) -3.2 (4.0) PA3038 probable porin -2.3 -3.5 (2.0) -4.4 (3.0) PA3174 probable transcriptional regulator -2.1 -3.5 (4.0) -6.5 (3.0) PA3205 hypothetical protein -1.3 -3.1 (4.0) -3.1 (4.0) PA3233 hypothetical protein -2.2 -2.7 (3.0) -5.1 (3.0) PA3234 probable sodium: solute symporter -4.5 -3.4 (2.0) -7.0 (3.0) PA3235 conserved hypothetical protein -3.9 -4.2 (3.0) -6.6 (3.0) PA3281 hypothetical protein -5.7 -6.4 (1.4) -24.9 (1.4) PA3282 hypothetical protein -8.5 -8.8 (1.4) -21.3 (1.4) PA3283 conserved hypothetical protein -9.0 -8.8 (1.4) -27.7 (1.4) PA3284 hypothetical protein -7.1 -10.4 (2.0) -24.3 (1.4) PA3364 amiC, aliphatic amidase expression-regulating protein -2.7 -1.8 (4.0) -2.7 (1.4) PA3365 probable chaperone -3.0 -1.7 (4.0) -4.0 (1.4) PA3575 hypothetical protein -1.6 -2.7 (1.4) -3.3 (2.0) PA3790 oprC, outer membrane protein OprC -2.7 -3.7 (2.0) -4.6 (2.0) PA4359 conserved hypothetical protein -1.4 -2.7 (2.0) -2.8 (1.4) PA4371 hypothetical protein -1.9 -4.1 (2.0) -2.8 (1.4) PA4442 cysN, ATP sulfurylase GTP-binding subunit -2.8 -3.4 (3.0) -7.6 (2.0) PA4443 cysD, ATP sulfurylase small subunit -3.1 -3.4 (3.0) -6.5 (2.0) PA4691 hypothetical protein -2.5 -2.8 (2.0) -2.9 (2.0) PA4692 conserved hypothetical protein -3.8 -3.4 (2.0) -5.0 (1.4) PA4770 lldP, L-lactate permease -1.8 -3.7 (2.0) -5.0 (2.0) PA5168 probable dicarboxylate transporter -2.7 -1.9 (4.0) -5.8 (2.0) .sup.aGene Identification Number from the Pseudomonas genome project (www.pseudomonas.com). .sup.bMaximum changes in gene expression (rounded to two significant figures) in the signal generation mutant in the presence of the signal(s) indicated compared with the absence of signal and in wild-type P. aeruginosa strain compared with the receptor mutant. The values in the parentheses are the OD.sub.600 at which the earliest change of .gtoreq.2.5 was observed (for the signal generation mutant, both time courses were considered). NC, no change. .sup.cThere is a las-rhl box-like sequence with an HI of .gtoreq.10 and <13.

[First Hit](#) [Fwd Refs](#)☐ [Generate Collection](#)[Print](#)

L9: Entry 6 of 9

File: USPT

Feb 20, 2001

US-PAT-NO: 6190667

DOCUMENT-IDENTIFIER: US 6190667 B1

TITLE: Methods of inhibiting Helicobacter pylori

DATE-ISSUED: February 20, 2001

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
De Reuse; Hilde	Paris			FR
Skouloubris; Stephane	Paris			FR
Cussac; Valerie	Paris			FR
Labigne; Agnes	Burress/Yvette			FR

US-CL-CURRENT: 424/234.1; 424/780, 435/32

CLAIMS:

We claim:

1. A method for screening a molecule capable of inhibiting the growth or survival of Helicobacter, comprising:

(a) contacting a parental Helicobacter strain with said molecule in a biological sample and contacting a Helicobacter strain deficient in UreI with said molecule;

(b) comparing the acidity sensitivity of the parental strain to the acidity sensitivity of the UreI deficient strain, both of which have been contacted with the molecule of step (a); and

(c) selecting said molecule that increases the acidity sensitivity of the parental strain as compared to the effect of said molecule on the acidity sensitivity of the UreI deficient strain, wherein acidity sensitivity is correlated with inhibiting Helicobacter growth or survival.

2. The method according to claim 1, wherein the acidity sensitivity is evaluated by measuring acidity resistance of the strains.

3. The method according to claim 1, wherein the molecule inhibits UreI activity.

4. The method according to claim 1, wherein the Helicobacter strain is selected from the group consisting of Helicobacter pylori, Helicobacter felis, Helicobacter helmannii, Helicobacter mustalae, Helicobacter canis, Helicobacter bilis, and Helicobacter hepaticus.

5. The method according to claim 1, wherein the molecule has a high affinity for UreI.

6. The method according to claim 1, wherein the molecule inhibits transport of urea or amide analogs.
7. The method according to claim 4, wherein the Helicobacter strain is Helicobacter pylori.
8. The method according to claim 1, wherein said Helicobacter strain deficient in UreI has wild type levels of urease activity.
9. The method according to claim 8, wherein the Helicobacter strain is Helicobacter pylori.
10. The method according to claim 9, wherein in step (b) acidity sensitivity is tested in the presence of urea.
11. The method according to claim 2, wherein acidity resistance is tested in the presence of urea.

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L9: Entry 5 of 9

File: USPT

Jun 19, 2001

DOCUMENT-IDENTIFIER: US 6248551 B1

TITLE: Helicobacter aliphatic amidase AmiE polypeptides, and DNA sequences encoding those polypeptidesAbstract Text (1):

This invention relates to Helicobacter species aliphatic amidase AmiE polypeptides, the DNA encoding those polypeptides and transformed microorganisms capable of expressing those polypeptides. This invention also relates to the use of Helicobacter sp. (particularly Helicobacter pylori) amidase AmiE polypeptides and antibodies specific for those polypeptides in immunogenic, therapeutic, and diagnostic applications. The invention additionally relates to processes of producing Helicobacter species aliphatic amidase AmiE polypeptides and intermediates intermediates useful in the production of those polypeptides.

Brief Summary Text (1):

This invention relates to Helicobacter species aliphatic amidase AmiE polypeptides, the DNA encoding those polypeptides, and transformed microorganisms capable of expressing those polypeptides. In addition, this invention relates to the use of Helicobacter sp. particularly Helicobacter pylori) amidase AmiE polypeptides and antibodies specific for those polypeptides in immunogenic, therapeutic and diagnostic application.

Brief Summary Text (3):

An aliphatic amidase is an acylamide amidohydrolase (E.C. 3.5.1.4) (Merck Index). It hydrolyses short-chain aliphatic amides (C1-C4 such as acrylamide, acetamide, propionamide or isobutyramide) to produce ammonia and the corresponding organic acid. In addition, an aliphatic amidase possesses acyl transferase activity, i.e., it is able to transfer the acyl group of amides to hydroxylamine to form an acyl hydroxamate plus ammonia.

Brief Summary Text (4):

Aliphatic amidases have been identified in Pseudomonas aeruginosa (Brammar et al., 1987) and Rhodococcus sp. R312 (previously named Brevibacterium sp. R312; Soubrier et al., 1992). Other aliphatic amidases have been identified in Methylophilus methylotrophus (Silman et al., 1991), Arthrobacter sp. J-1 (Asano et al., 1982), and Alcaligenes eutrophus (Friedrich and Mitrenga, 1981). However, no molecular characterization of these latter three enzymes has been reported.

Brief Summary Text (5):

Aliphatic amidases are cytoplasmic enzymes; they have very similar enzymatic properties and molecular masses (38.4 kDa for P. aeruginosa; 38.2 kDa for Rhodococcus sp. R312; 37.8 kDa for M. methylotrophus; and 39 kDa for Arthrobacter sp. J-1), and have either a tetra-, hexa-, or octameric structure. Some of these amidases have been shown to be inducible by their amide substrate. Database searches with the amino acid sequences of these aliphatic amidases indicates that they are more closely related to nitrilases (which catalyze the direct cleavage of nitrites to ammonia and to the corresponding acid) than to the nitrile hydratases (which hydrolyze nitrites to produce amides) or amidases from other classes (Novo et al., 1995).

Status: Signed Off. (6 minutes)

Status: Path 1 of [Dialog Information Services via Modem]

Status: Initializing TCP/IP using (UseTelnetProto 1 ServiceID pto-dialog)
Trying 31060000009999...Open

DIALOG INFORMATION SERVICES

PLEASE LOGON:

***** HHHHHHHH SSSSSSS?

Status: Signing onto Dialog

ENTER PASSWORD:

***** HHHHHHHH SSSSSSS? *****

Welcome to DIALOG

Status: Connected

Dialog level 04.02.00D

Last logoff: 13apr04 11:40:01

Logon file405 13apr04 12:03:16

*

*

* ALL NEW CURRENT YEAR RANGES HAVE BEEN * * *

* * * INSTALLED * * *

SYSTEM:HOME

Cost is in DialUnits

Menu System II: D2 version 1.7.9 term=ASCII

*** DIALOG HOMEBASE(SM) Main Menu ***

Information:

1. Announcements (new files, reloads, etc.)
2. Database, Rates, & Command Descriptions
3. Help in Choosing Databases for Your Topic
4. Customer Services (telephone assistance, training, seminars, etc.)
5. Product Descriptions

Connections:

6. DIALOG(R) Document Delivery
7. Data Star(R)

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/H = Help

/L = Logoff

/NOMENU = Command Mode

Enter an option number to view information or to connect to an online service. Enter a BEGIN command plus a file number to search a database (e.g., B1 for ERIC).

? b 155 medicine

13apr04 12:03:21 User228206 Session D2146.1

\$0.00 0.153 DialUnits FileHomeBase

\$0.00 Estimated cost FileHomeBase

\$0.02 TELNET

\$0.02 Estimated cost this search

\$0.02 Estimated total session cost 0.153 DialUnits

SYSTEM:OS - DIALOG OneSearch

File 155:MEDLINE(R) 1966-2004/Apr W1

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***File 155: Medline has been reloaded. Accession numbers have changed. Please see HELP NEWS 154 for details.**

File 5:Biosis Previews(R) 1969-2004/Apr W1

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File 34:SciSearch(R) Cited Ref Sci 1990-2004/Apr W1
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File 35:Dissertation Abs Online 1861-2004/Mar
(c) 2004 ProQuest Info&Learning
File 48:SPORTDiscus 1962-2004/Mar
(c) 2004 Sport Information Resource Centre
File 65:Inside Conferences 1993-2004/Apr W1
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(c) 2004 Elsevier Science B.V.
File 73:EMBASE 1974-2004/Apr W1
(c) 2004 Elsevier Science B.V.
File 91:MANTIS(TM) 1880-2003/Aug
2001 (c) Action Potential
File 94:JICST-EPlus 1985-2004/Mar W4
(c)2004 Japan Science and Tech Corp (JST)
File 98:General Sci Abs/Full-Text 1984-2004/Apr
(c) 2004 The HW Wilson Co.
File 135:NewsRx Weekly Reports 1995-2004/Apr W1
(c) 2004 NewsRx
***File 135: New newsletters are now added. See Help News135 for the complete list of newsletters.**
File 144:Pascal 1973-2004/Apr W1
(c) 2004 INIST/CNRS
File 149:TGG Health&Wellness DB(SM) 1976-2004/Apr W1
(c) 2004 The Gale Group
File 156:ToxFile 1965-2004/Apr W2
(c) format only 2004 The Dialog Corporation
File 159:Cancerlit 1975-2002/Oct
(c) format only 2002 Dialog Corporation
***File 159: Cancerlit ceases updating with immediate effect.**
Please see HELP NEWS.
File 162:Global Health 1983-2004/Mar
(c) 2004 CAB International
File 164:Allied & Complementary Medicine 1984-2004/Apr
(c) 2004 BLHCIS
File 172:EMBASE Alert 2004/Apr W1
(c) 2004 Elsevier Science B.V.
File 266:FEDRIP 2004/Feb
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File 369:New Scientist 1994-2004/Apr W1
(c) 2004 Reed Business Information Ltd.
File 370:Science 1996-1999/Jul W3
(c) 1999 AAAS
***File 370: This file is closed (no updates). Use File 47 for more current information.**
File 399:CA SEARCH(R) 1967-2004/UD=14016
(c) 2004 American Chemical Society
***File 399: Use is subject to the terms of your user/customer agreement.**
Alert feature enhanced for multiple files, etc. See HELP ALERT.
File 434:SciSearch(R) Cited Ref Sci 1974-1989/Dec
(c) 1998 Inst for Sci Info
File 444:New England Journal of Med. 1985-2004/Apr W2
(c) 2004 Mass. Med. Soc.
File 467:ExtraMED(tm) 2000/Dec
(c) 2001 Informania Ltd.
***File 467: For information about updating status please see Help News467.**

Set Items Description

?e aliphatic amidase

Ref	Items	RT	Index-term
E1	34		*ALIPHATIC AMIDASE
E2	1		ALIPHATIC AMIDASE AMIE
E3	1		ALIPHATIC AMIDASE OPERON
E4	3		ALIPHATIC AMIDASES
E5	2	1	ALIPHATIC AMIDE

E6	1	ALIPHATIC AMIDE FEED SUPPLEMENT
E7	47	ALIPHATIC AMIDES
E8	1	ALIPHATIC AMIDES METAL CHELATING AGENTS IRON C
E9	0	1 ALIPHATIC AMIDINE
E10	54717	218 ALIPHATIC AMINE
E11	7	ALIPHATIC AMINE --ADVERSE DRUG REACTION --AE
E12	3	ALIPHATIC AMINE --CLINICAL TRIAL --CT

Enter P or PAGE for more

?p

Ref	Items	Index-term
E13	1	ALIPHATIC AMINE --DRUG ADMINISTRATION --AD
E14	67	ALIPHATIC AMINE --DRUG ANALYSIS --AN
E15	4	ALIPHATIC AMINE --DRUG COMBINATION --CB
E16	23	ALIPHATIC AMINE --DRUG COMPARISON --CM
E17	1	ALIPHATIC AMINE --DRUG CONCENTRATION --CR
E18	60	ALIPHATIC AMINE --DRUG DEVELOPMENT --DV
E19	5	ALIPHATIC AMINE --DRUG DOSE --DO
E20	2	ALIPHATIC AMINE --DRUG INTERACTION --IT
E21	22	ALIPHATIC AMINE --DRUG THERAPY --DT
E22	44	ALIPHATIC AMINE --DRUG TOXICITY --TO
E23	11	ALIPHATIC AMINE --ENDOGENOUS COMPOUND --EC
E24	1	ALIPHATIC AMINE --INTRADERMAL DRUG ADMINISTRATION

Enter P or PAGE for more

?s e1-e4

34	ALIPHATIC AMIDASE
1	ALIPHATIC AMIDASE AMIE
1	ALIPHATIC AMIDASE OPERON
3	ALIPHATIC AMIDASES

S1 39 E1-E4

?t s1/free/all

>>>"FREE" is not a valid format name in file(s): 399

1/8/1 (Item 1 from file: 5)
0013460258 BIOSIS NO.: 200200053769
The Helicobacter pylori paralogous amidases: Analysis of their role in vivo and distribution of amiE/amiF among Helicobacter species
2001

1/8/2 (Item 2 from file: 5)
0013332021 BIOSIS NO.: 200100503860
Aliphatic and enantioselective amidases: From hydrolysis to acyl transfer activity
2001

1/8/3 (Item 3 from file: 5)
0013215382 BIOSIS NO.: 200100387221
Helicobacter aliphatic amidase AmiE polypeptides, and DNA sequences encoding those polypeptides
2001

1/8/4 (Item 4 from file: 5)
0013183385 BIOSIS NO.: 200100355224
Substitutions of Thr-103-Ile and Trp-138-Gly in amidase from Pseudomonas aeruginosa are responsible for altered kinetic properties and enzyme instability
2001

1/8/5 (Item 5 from file: 5)
0013105593 BIOSIS NO.: 200100277432
The AmiE aliphatic amidase and AmiF formamidase of Helicobacter pylori: Natural evolution of two enzyme paralogues
2001

1/8/6 (Item 6 from file: 5)
0012979581 BIOSIS NO.: 200100151420
Comparative RNA expression profiling analysis of *Helicobacter pylori*
wild-type and *cadA* ATPase mutants employing whole genome microarrays
detects genes physiologically linked to heavy metal resistance in gastric
bacteria
2000

1/8/7 (Item 7 from file: 5)
0012651169 BIOSIS NO.: 200000369482
Crystal structure of N-carbamyl-D-amino acid amidohydrolase with a novel
catalytic framework common to amidohydrolases
2000

1/8/8 (Item 8 from file: 5)
0012290079 BIOSIS NO.: 200000008392
Crystal structure and induction mechanism of AmiC-AmiR: A ligand-regulated
transcription antitermination complex
1999

1/8/9 (Item 9 from file: 5)
0012248978 BIOSIS NO.: 199900508638
Amino acid homologies between human biotinidase and bacterial aliphatic
amidases: Putative identification of the active site of biotinidase
1999

1/8/10 (Item 10 from file: 5)
0011231256 BIOSIS NO.: 199800025503
The aliphatic amidase: Another way to produce ammonia in *H. pylori*?
1997

1/8/11 (Item 11 from file: 5)
0011157503 BIOSIS NO.: 199799791563
Identification and characterization of an aliphatic amidase in *Helicobacter*
pylori
1997

1/8/12 (Item 12 from file: 5)
0010836795 BIOSIS NO.: 199799470855
A *Pseudomonas putida* capable of stereoselective hydrolysis of nitriles
1997

1/8/13 (Item 13 from file: 5)
0010370983 BIOSIS NO.: 199699005043
Characterization of the gene cluster of high-molecular-mass nitrile
hydratase (H-NHase) induced by its reaction product in *Rhodococcus*
rhodochrous J1
1996

1/8/14 (Item 14 from file: 5)
0009473435 BIOSIS NO.: 199497494720
A new family carbon-nitrogen hydrolases
1994

1/8/15 (Item 1 from file: 34)
DIALOG(R)File 34:(c) 2004 Inst for Sci Info. All rts. reserv.

12480083 Genuine Article#: 771BV Number of References: 43

Title: Acid-responsive gene induction of ammonia-producing enzymes in Helicobacter pylori is mediated via a metal-responsive repressor cascade (ABSTRACT AVAILABLE)

Publication date: 20040200

Journal Subject Category: IMMUNOLOGY; INFECTIOUS DISEASES

Identifiers--KeyWord Plus(R): FERRIC UPTAKE REGULATOR; UREASE ACTIVITY; LOW-PH; **ALIPHATIC AMIDASE**; PHASE VARIATION; EXPRESSION; IDENTIFICATION; PROTEIN; NIKR; FUR

1/8/16 (Item 2 from file: 34)

DIALOG(R)File 34:(c) 2004 Inst for Sci Info. All rts. reserv.

12266057 Genuine Article#: 747ZE Number of References: 47

Title: Burkholderia genome analysis reveals new enzymes belonging to the nitrilase superfamily - The amidase of Burkholderia cepacia (hospital isolate) (ABSTRACT AVAILABLE)

Publication date: 20031200

Journal Subject Category: BIOCHEMISTRY & MOLECULAR BIOLOGY

Descriptors--Author Keywords: Burkholderia genome ; amidase ; nitrilase superfamily

Identifiers--KeyWord Plus(R): PSEUDOMONAS-AERUGINOSA AMIDASE; AMINO-ACID AMIDOHYDROLASE; SITE-DIRECTED MUTAGENESIS; WIDE-SPECTRUM AMIDASE; SUBSTRATE-SPECIFICITY; **ALIPHATIC AMIDASE**; CRYSTAL-STRUCTURE; ESCHERICHIA-COLI; SWISS-MODEL; ACTIVE-SITE

1/8/17 (Item 3 from file: 34)

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12230215 Genuine Article#: 744CM Number of References: 25

Title: Measuring enzymatic activity of a recombinant amidase using Fourier transform infrared spectroscopy (ABSTRACT AVAILABLE)

Publication date: 20031115

Journal Subject Category: BIOCHEMICAL RESEARCH METHODS; BIOCHEMISTRY & MOLECULAR BIOLOGY; CHEMISTRY, ANALYTICAL

Descriptors--Author Keywords: recombinant amidase ; Fourier transform-infrared spectroscopy (FT-IR) ; enzymatic activity ; hydrolysis ; acetamide

Identifiers--KeyWord Plus(R): PSEUDOMONAS AERUGINOSA AMIDASE; **ALIPHATIC AMIDASE**; ASSAY; PURIFICATION; ACETAMIDE; UREA

1/8/18 (Item 4 from file: 34)

DIALOG(R)File 34:(c) 2004 Inst for Sci Info. All rts. reserv.

11471559 Genuine Article#: 654YF Number of References: 48

Title: Differential regulation of amidase- and formamidase-mediated ammonia production by the Helicobacter pylori fur repressor (ABSTRACT AVAILABLE)

Publication date: 20030314

Journal Subject Category: BIOCHEMISTRY & MOLECULAR BIOLOGY

Identifiers--KeyWord Plus(R): FERRIC UPTAKE REGULATOR; UREASE ACTIVITY; GASTRIC COLONIZATION; **ALIPHATIC AMIDASE**; MAILLARD REACTION; ACID RESISTANCE; IDENTIFICATION; PROTEIN; TRANSCRIPTION; EXPRESSION

1/8/19 (Item 5 from file: 34)

DIALOG(R)File 34:(c) 2004 Inst for Sci Info. All rts. reserv.

10899399 Genuine Article#: 582RR Number of References: 49

Title: Support for a three-dimensional structure predicting a Cys-Glu-Lys catalytic triad for Pseudomonas aeruginosa amidase comes from site-directed mutagenesis and mutations altering substrate specificity (ABSTRACT AVAILABLE)

Publication date: 20020801

Journal Subject Category: BIOCHEMISTRY & MOLECULAR BIOLOGY

Descriptors--Author Keywords: comparative modelling ; NitFhit ; nitrilase
Identifiers--KeyWord Plus(R): WIDE-SPECTRUM AMIDASE; ACTIVE-SITE;

ALIPHATIC AMIDASE; CRYSTAL-STRUCTURE; SWISS-MODEL; NITRILASE; CLONING; ENZYME; PROTEINS; DOCKING

1/8/20 (Item 6 from file: 34)

DIALOG(R)File 34:(c) 2004 Inst for Sci Info. All rts. reserv.

10782796 Genuine Article#: 569YV Number of References: 68

Title: Cloning and heterologous expression of an enantio selective amidase from Rhodococcus erythropolis strain MP50 (ABSTRACT AVAILABLE)

Publication date: 20020700

Journal Subject Category: BIOTECHNOLOGY & APPLIED MICROBIOLOGY; MICROBIOLOGY

Identifiers--KeyWord Plus(R): PSEUDOMONAS-CHLORORAPHIS B23; MASS NITRILE HYDRATASE; ENANTIOSELECTIVE HYDROLYSIS; METHYLOPHILUS-METHYLOTROPHUS; NUCLEOTIDE-SEQUENCE; STRUCTURAL EVIDENCE; **ALIPHATIC AMIDASE**; ESCHERICHIA-COLI; NAPROXEN AMIDE; RHODOCHROUS J1

1/8/21 (Item 7 from file: 34)

DIALOG(R)File 34:(c) 2004 Inst for Sci Info. All rts. reserv.

10087744 Genuine Article#: 483HR Number of References: 19

Title: A monoclonal antibody specific for Pseudomonas aeruginosa amidase (ABSTRACT AVAILABLE)

Publication date: 20010800

Journal Subject Category: BIOCHEMICAL RESEARCH METHODS; BIOTECHNOLOGY & APPLIED MICROBIOLOGY; IMMUNOLOGY

Identifiers--KeyWord Plus(R): WIDE-SPECTRUM AMIDASE; DIRECTED EVOLUTION; **ALIPHATIC AMIDASE**; ACTIVE-SITE; PURIFICATION; SEQUENCE; CLONING; FAMILY; ENZYME

1/8/22 (Item 8 from file: 34)

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09783237 Genuine Article#: 448XY Number of References: 42

Title: Molecular and biochemical characterization of the recombinant amidase from hyperthermophilic archaeon Sulfolobus solfataricus (ABSTRACT AVAILABLE)

Publication date: 20010600

Journal Subject Category: BIOCHEMISTRY & MOLECULAR BIOLOGY; MICROBIOLOGY

Descriptors--Author Keywords: Sulfolobus solfataricus ; Archaea ; amidase ; signatred amidase ; thermophiles

Identifiers--KeyWord Plus(R): ENANTIOMER-SELECTIVE AMIDASE; COMPLETE GENOME SEQUENCE; ACYL TRANSFER ACTIVITY; AMINO-ACID SEQUENCE; NITRILE HYDRATASE; PSEUDOMONAS-AERUGINOSA; STRUCTURAL EVIDENCE; **ALIPHATIC AMIDASE**; ESCHERICHIA-COLI; PURIFICATION

1/8/23 (Item 9 from file: 34)

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09030994 Genuine Article#: 358VM Number of References: 32

Title: Steric hindrance regulation of the Pseudomonas aeruginosa amidase operon (ABSTRACT AVAILABLE)

Publication date: 20000929

Journal Subject Category: BIOCHEMISTRY & MOLECULAR BIOLOGY

Identifiers--KeyWord Plus(R): BINDING ATTENUATION PROTEIN; NIFL-NIFA COMPLEX; TRANSCRIPTION ANTITERMINATION; **ALIPHATIC AMIDASE**; NUCLEOTIDE-SEQUENCE; NITROGEN-FIXATION; CRYSTAL-STRUCTURE; GENE AMIR; RNA; EXPRESSION

1/8/24 (Item 10 from file: 34)

DIALOG(R)File 34:(c) 2004 Inst for Sci Info. All rts. reserv.

08553508 Genuine Article#: 299TF Number of References: 32

Title: Amino acid homologies between human biotinidase and bacterial

aliphatic amidases: Putative identification of the active site of biotinidase (ABSTRACT AVAILABLE)

Publication date: 20000200

Journal Subject Category: GENETICS & HEREDITY; MEDICINE, RESEARCH & EXPERIMENTAL; BIOCHEMISTRY & MOLECULAR BIOLOGY

Descriptors--Author Keywords: biotinidase ; **aliphatic amidase** ; nitrilase ; active site

Identifiers--KeyWord Plus(R): HUMAN-SERUM BIOTINIDASE; PSEUDOMONAS-AERUGINOSA; COMMON-CAUSE; DEFICIENCY; GENE; NITRILASE; CLONING; BIOSYNTHESIS; PURIFICATION; SEQUENCE

1/8/25 (Item 11 from file: 34)

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08534599 Genuine Article#: 297HP Number of References: 21

Title: Structural adaptation to selective pressure for altered ligand specificity in the Pseudomonas aeruginosa amide receptor, AmiC (ABSTRACT AVAILABLE)

Publication date: 20000200

Journal Subject Category: BIOTECHNOLOGY & APPLIED MICROBIOLOGY; BIOCHEMISTRY & MOLECULAR BIOLOGY

Descriptors--Author Keywords: crystallography ; ligand specificity ; mutation ; protein evolution ; small molecule binding protein

Identifiers--KeyWord Plus(R): TRANSCRIPTION ANTITERMINATION; **ALIPHATIC AMIDASE**; BINDING-PROTEIN; CRYSTALLIZATION; OPERON; EXPRESSION; ERRORS; GENES; MAPS

1/8/26 (Item 12 from file: 34)

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07798176 Genuine Article#: 209UB Number of References: 23

Title: Evidence that cysteine-166 is the active-site nucleophile of Pseudomonas aeruginosa amidase: crystallization and preliminary X-ray diffraction analysis of the enzyme (ABSTRACT AVAILABLE)

Publication date: 19990615

Journal Subject Category: BIOCHEMISTRY & MOLECULAR BIOLOGY

Identifiers--KeyWord Plus(R): **ALIPHATIC AMIDASE**; IDENTIFICATION; PURIFICATION; NITRILASE; SEQUENCE; FAMILY; GENE

1/8/27 (Item 13 from file: 34)

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05333966 Genuine Article#: VR218 Number of References: 25

Title: TRANSCRIPTION ANTITERMINATION REGULATION OF THE PSEUDOMONAS-AERUGINOSA AMIDASE OPERON (Abstract Available)

Journal Subject Category: BIOCHEMISTRY & MOLECULAR BIOLOGY; CELL BIOLOGY

Descriptors--Author Keywords: AMIDASE ; ANTITERMINATION ; PSEUDOMONAS-AERUGINOSA

Identifiers--KeyWords Plus: **ALIPHATIC AMIDASE**; CRYSTAL-STRUCTURE; ESCHERICHIA-COLI; BGL OPERON; GENE AMIR; RNA; EXPRESSION; SEQUENCE; PHOSPHORYLATION; TERMINATION

Research Fronts: 94-3167 002 (RNA FOLDING; SEQUENCE DEPENDENCE OF STABILITY; SECONDARY STRUCTURE MODEL; HIV-1 VIRUS)

94-4806 001 (GENE ORGANIZATION; LONG-CHAIN FATTY-ACID TRANSPORT; TRANSCRIPTION FACTOR)

1/8/28 (Item 14 from file: 34)

DIALOG(R)File 34:(c) 2004 Inst for Sci Info. All rts. reserv.

05199091 Genuine Article#: VG565 Number of References: 38

Title: MOLECULAR CHARACTERIZATION OF FORMAMIDASE FROM METHYLOPHILUS-METHYLOTROPHUS (Abstract Available)

Journal Subject Category: BIOCHEMISTRY & MOLECULAR BIOLOGY

Descriptors--Author Keywords: FORMAMIDASE ; FMDA ; FMDB ; METHYLOPHILUS METHYLOTROPHUS

Identifiers--KeyWords Plus: ENANTIOMER-SELECTIVE AMIDASE; PROTEIN SECONDARY STRUCTURE; PSEUDOMONAS-AERUGINOSA; NITRILE HYDRATASE; METHANOL DEHYDROGENASE; NUCLEOTIDE-SEQUENCE; CONTINUOUS CULTURE; **ALIPHATIC AMIDASE**; BINDING-PROTEIN; GENE
Research Fronts: 94-4806 001 (GENE ORGANIZATION; LONG-CHAIN FATTY-ACID TRANSPORT; TRANSCRIPTION FACTOR)

1/8/29 (Item 15 from file: 34)
DIALOG(R)File 34:(c) 2004 Inst for Sci Info. All rts. reserv.

04402358 Genuine Article#: TA647 Number of References: 26
Title: REGULATION OF NITROGEN-METABOLISM, STARCH UTILIZATION AND THE BETA-HBD-ADHL GENE-CLUSTER IN CLOSTRIDIUM-ACETOBUTYLICUM (Abstract Available)
Journal Subject Category: MICROBIOLOGY
Descriptors--Author Keywords: GENE REGULATION ; CLOSTRIDIUM ACETOBUTYLICUM ; GLUTAMINE SYNTHETASE ; CCPA GENE ; ADHL GENE ; P-HBD GENE
Identifiers--KeyWords Plus: PSEUDOMONAS-AERUGINOSA; BACILLUS-SUBTILIS; NUCLEOTIDE-SEQUENCE; MOLECULAR ANALYSIS; GLUTAMINE-SYNTHETASE; **ALIPHATIC AMIDASE**; EXPRESSION; ANTITERMINATION; ENZYMES; ACETATE

1/8/30 (Item 16 from file: 34)
DIALOG(R)File 34:(c) 2004 Inst for Sci Info. All rts. reserv.

04198272 Genuine Article#: RN954 Number of References: 41
Title: IDENTIFICATION OF 2 NEW GENES IN THE PSEUDOMONAS-AERUGINOSA AMIDASE OPERON, ENCODING AN ATPASE (AMIB) AND A PUTATIVE INTEGRAL MEMBRANE-PROTEIN (AMIS) (Abstract Available)
Journal Subject Category: BIOCHEMISTRY & MOLECULAR BIOLOGY
Identifiers--KeyWords Plus: ESCHERICHIA-COLI; NUCLEOTIDE-SEQUENCE; **ALIPHATIC AMIDASE**; BINDING PROTEIN; EXPRESSION; CLONING; PURIFICATION; COMPONENTS; PRODUCT; SUBUNIT
Research Fronts: 93-4847 002 (HETEROLOGOUS EXPRESSION; CHROMOSOMAL DNA; GENE ENCODING METHYLMALONYL-COENZYME-A MUTASE)
93-3088 001 (RAT MUSCLE; PROTEIN PHOSPHATASE-1; MAJOR GLUTATHIONE TRANSFERASE)
93-8105 001 (PUTATIVE CATALYTIC ATP-BINDING SITE OF THE BACILLUS-SUBTILIS SECA PROTEIN; CONSERVED MOTIFS; INDEPENDENT DOMAINS)

1/8/31 (Item 17 from file: 34)
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04035936 Genuine Article#: RA622 Number of References: 23
Title: TRANSCRIPTIONAL ANALYSIS OF THE AMIDASE OPERON FROM PSEUDOMONAS-AERUGINOSA (Abstract Available)
Journal Subject Category: MICROBIOLOGY
Identifiers--KeyWords Plus: **ALIPHATIC AMIDASE**; CATABOLITE REPRESSION; NUCLEOTIDE-SEQUENCE; ESCHERICHIA-COLI; AMIE GENE; EXPRESSION; DNA; COMPLEMENTATION; CLONING; PRODUCT
Research Fronts: 93-4847 002 (HETEROLOGOUS EXPRESSION; CHROMOSOMAL DNA; GENE ENCODING METHYLMALONYL-COENZYME-A MUTASE)

1/8/32 (Item 18 from file: 34)
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03080704 Genuine Article#: ND468 Number of References: 22
Title: ARG-188 AND TRP-144 ARE IMPLICATED IN THE BINDING OF UREA AND ACETAMIDE TO THE ACTIVE-SITE OF THE AMIDASE FROM PSEUDOMONAS-AERUGINOSA (Abstract Available)
Journal Subject Category: BIOCHEMISTRY & MOLECULAR BIOLOGY; BIOPHYSICS
Descriptors--Author Keywords: AMIDASE ; UREA BINDING ; MUTATION ; ACETANILIDASE ; (PSEUDOMONAS-AERUGINOSA)
Identifiers--KeyWords Plus: **ALIPHATIC AMIDASE**; SEQUENCE

1/8/33 (Item 19 from file: 34)
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02658267 Genuine Article#: LU513 Number of References: 31
**Title: ANTITERMINATION OF AMIDASE EXPRESSION IN PSEUDOMONAS-AERUGINOSA IS
CONTROLLED BY A NOVEL CYTOPLASMIC AMIDE-BINDING PROTEIN** (Abstract
Available)
Journal Subject Category: BIOCHEMISTRY & MOLECULAR BIOLOGY
Descriptors--Author Keywords: BINDING PROTEINS ; GENE REGULATION ; SIGNAL
TRANSDUCTION
Identifiers--KeyWords Plus: ESCHERICHIA-COLI; NUCLEOTIDE-SEQUENCE;
TRANSCRIPTIONAL ANTITERMINATION; SALMONELLA-TYPHIMURIUM; **ALIPHATIC
AMIDASE;** BGL OPERON; GENE AMIR; CLONING; TRANSPORT; ALIGNMENT

1/8/34 (Item 20 from file: 34)
DIALOG(R)File 34:(c) 2004 Inst for Sci Info. All rts. reserv.

01314772 Genuine Article#: GN696 Number of References: 16
**Title: N-TERMINAL AMINO-ACID-SEQUENCE OF BREVIBACTERIUM SP R312
WIDE-SPECTRUM AMIDASE** (Abstract Available)
Journal Subject Category: BIOTECHNOLOGY & APPLIED MICROBIOLOGY;
MICROBIOLOGY
Identifiers--KeyWords Plus: NITRILE HYDRATASE; PSEUDOMONAS-AERUGINOSA;
ALIPHATIC AMIDASE; SP STRAIN-R312; PURIFICATION
Research Fronts: 89-3034 001 (MICROTUBULE CROSS-LINKING PROTEIN; SMALL
SYNAPTIC VESICLES OF RAT-BRAIN; AXOLININ LOCALIZATION)

1/8/35 (Item 1 from file: 71)
01404571 2000080041
**Amino acid homologies between human biotinidase and bacterial aliphatic
amidases: Putative identification of the active site of biotinidase**

1/8/36 (Item 1 from file: 73)
03918813 EMBASE No: 1989087806
**Nucleotide sequence of the aliphatic amidase regulator gene (amiR) of
Pseudomonas aeruginosa**
1989

1/8/37 (Item 2 from file: 73)
01715617 EMBASE No: 1980083910
Local anesthetics block induction of the Pseudomonas alk regulon
1979

1/8/38 (Item 3 from file: 73)
01507397 EMBASE No: 1979229151
**Inhibition of the aliphatic amidase from Pseudomonas aeruginosa by urea
and related compounds**
1979

1/8/39 (Item 4 from file: 73)
00936651 EMBASE No: 1978064941
**Relationship between culture density and catabolite repression of an
inducible aliphatic amidase in a thermophilic bacillus**
1977
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\$0.05 Estimated cost File155
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$0.30 Estimated cost File434
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    $0.13 0.020 DialUnits File467
$0.13 Estimated cost File467
    OneSearch, 26 files, 0.782 DialUnits FileOS
$0.24 TELNET
$7.97 Estimated cost this search
$7.99 Estimated total session cost 0.935 DialUnits

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Status: Path 1 of [Dialog Information Services via Modem]

Status: Initializing TCP/IP using (UseTelnetProto 1 ServiceID pto-dialog)
Trying 31060000009999...Open

DIALOG INFORMATION SERVICES
PLEASE LOGON:

***** HHHHHHHH SSSSSSSS?
Status: Signing onto Dialog

ENTER PASSWORD:
***** HHHHHHHH SSSSSSSS? *****
Welcome to DIALOG
Status: Connected

Dialog level 04.02.00D

Reconnected in file OS 13apr04 12:08:45

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* ALL NEW CURRENT YEAR RANGES HAVE BEEN * * *
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File 155:MEDLINE(R) 1966-2004/Apr W1
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have changed. Please see HELP NEWS 154 for details.
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File 73:EMBASE 1974-2004/Apr W1
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File 91:MANTIS(TM) 1880-2003/Aug
2001 (c) Action Potential
File 94:JICST-EPlus 1985-2004/Mar W4
(c) 2004 Japan Science and Tech Corp(JST)
File 98:General Sci Abs/Full-Text 1984-2004/Apr
(c) 2004 The HW Wilson Co.
File 135:NewsRx Weekly Reports 1995-2004/Apr W1
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complete list of newsletters.
File 144:Pascal 1973-2004/Apr W1
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File 149:TGG Health&Wellness DB(SM) 1976-2004/Apr W1
(c) 2004 The Gale Group
File 156:ToxFile 1965-2004/Apr W2
(c) format only 2004 The Dialog Corporation
File 159:Cancerlit 1975-2002/Oct
(c) format only 2002 Dialog Corporation
*File 159: Cancerlit ceases updating with immediate effect.
Please see HELP NEWS.
File 162:Global Health 1983-2004/Mar
(c) 2004 CAB International
File 164:Allied & Complementary Medicine 1984-2004/Apr
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(c) 2004 Elsevier Science B.V.
File 266:FEDRIP 2004/Feb
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File 369:New Scientist 1994-2004/Apr W1
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File 370:Science 1996-1999/Jul W3
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File 399:CA SEARCH(R) 1967-2004/UD=14016

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File 434:SciSearch(R) Cited Ref Sci 1974-1989/Dec

(c) 1998 Inst for Sci Info

File 444:New England Journal of Med. 1985-2004/Apr W2

(c) 2004 Mass. Med. Soc.

File 467:ExtraMED(tm) 2000/Dec

(c) 2001 Informania Ltd.

*File 467: For information about updating status please see Help News467.

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DATE: Tuesday, April 13, 2004

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<input type="checkbox"/>	L1	(chloroacetone or chloro-acetone).clm.	29
<input type="checkbox"/>	L2	L1 same (method or process)	21
<input type="checkbox"/>	L3	L1 same (method or process).clm.	21
<input type="checkbox"/>	L4	(amidase or aliphatic).clm. same (method or process).clm.	20641
<input type="checkbox"/>	L5	L4 and (treat\$ or prevent\$ or therapeut\$ or inhibit\$ or modulat\$ or block\$ or inactiv\$ or antagon\$).clm.	5184
<input type="checkbox"/>	L6	L4 same (treat\$ or prevent\$ or therapeut\$ or inhibit\$ or modulat\$ or block\$ or inactiv\$ or antagon\$).clm.	1601
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END OF SEARCH HISTORY

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File 5:Biosis Previews(R) 1969-2004/Apr W1

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File 399:CA SEARCH(R) 1967-2004/UD=14016

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File 440:Current Contents Search(R) 1990-2004/Apr 13

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File 144:Pascal 1973-2004/Apr W1

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File 357:Derwent Biotech Res. 1982-2004/Apr W2

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File 340:CLAIMS(R)/US Patent 1950-04/Apr 08

(c) 2004 IFI/CLAIMS(R)

*File 340: Annual reload and classification updates delayed due to processing issues.

File 654:US Pat.Full. 1976-2004/Apr 06

(c) Format only 2004 The Dialog Corp.

*File 654: US published applications now online. See HELP NEWS 654 for details. Reassignments current through December 2, 2003.

File 143:Biol. & Agric. Index 1983-2004/Mar

(c) 2004 The HW Wilson Co

File 156:ToxFile 1965-2004/Apr W2

(c) format only 2004 The Dialog Corporation

File 50:CAB Abstracts 1972-2004/Mar

(c) 2004 CAB International

File 65:Inside Conferences 1993-2004/Apr W1

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File 203:AGRIS 1974-2004/Feb

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File 342:Derwent Patents Citation Indx 1978-04/200420

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File 348:EUROPEAN PATENTS 1978-2004/Apr W01

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File 349:PCT FULLTEXT 1979-2002/UB=20040408,UT=20040401

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S1 127 ALIPHATIC?/TI AND AMIDASE?/TI

S2 48 RD (unique items)

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2/9/1 (Item 1 from file: 155)

DIALOG(R)File 155:MEDLINE(R)

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13675690 PMID: 9364923

Identification and characterization of an aliphatic amidase in *Helicobacter pylori*.

Skouloubris S; Labigne A; De Reuse H

Unite de Pathogenie Bacterienne des Muqueuses, Institut Pasteur, Paris, France.

Molecular microbiology (ENGLAND) Sep 1997, 25 (5) p989-98, ISSN

0950-382X Journal Code: 8712028

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

We report, for the first time, the presence in *Helicobacter pylori* of an aliphatic amidase that, like urease, contributes to ammonia production. Aliphatic amidases are cytoplasmic acylamide amidohydrolases (EC 3.5.1.4) hydrolysing short-chain aliphatic amides to produce ammonia and the corresponding organic acid. The finding of an aliphatic amidase in *H. pylori* was unexpected as this enzyme has only previously been described in bacteria of environmental (soil or water) origin. The *H. pylori* amidase gene *amiE* (1017 bp) was sequenced, and the deduced amino acid sequence of *AmiE* (37746Da) is very similar (75% identity) to the other two sequenced aliphatic amidases, one from *Pseudomonas aeruginosa* and one from *Rhodococcus* sp. R312. Amidase activity was measured as the release of ammonia by sonicated crude extracts from *H. pylori* strains and from recombinant *Escherichia coli* strains overproducing the *H. pylori* amidase. The substrate specificity was analysed with crude extracts from *H. pylori* cells grown in vitro; the best substrates were propionamide, acrylamide and acetamide. Polymerase chain reaction (PCR) amplification of an internal *amiE* sequence was obtained with each of 45 different *H. pylori* clinical isolates, suggesting that amidase is common to all *H. pylori* strains. A *H. pylori* mutant (N6-836) carrying an interrupted *amiE* gene was constructed by allelic exchange. No amidase activity could be detected in N6-836. In a N6-urease negative mutant, amidase activity was two- to threefold higher than in the parental strain N6. Crude extracts of strain N6 slowly hydrolysed formamide. This activity was affected in neither the amidase negative strain (N6-836) nor a double mutant strain deficient in both amidase and urease activities, suggesting the presence of an independent discrete formamidase in *H. pylori*. The existence of an aliphatic amidase, a correlation between the urease and amidase activities and the possible presence of a formamidase indicates that *H. pylori* has a large range of possibilities for intracellular ammonia production.

Tags: Comparative Study; Support, Non-U.S. Gov't

Descriptors: *Amidohydrolases--analysis--AN; **Helicobacter pylori* --enzymology--EN; Amino Acid Sequence; Cloning, Molecular; DNA, Recombinant; *Escherichia coli*--enzymology--EN; *Escherichia coli*--genetics--GE; Genes, Structural, Bacterial--genetics--GE; *Helicobacter pylori*--chemistry--CH; *Helicobacter pylori*--genetics--GE; Molecular Sequence Data; Mutation --genetics--GE; Recombinant Proteins--genetics--GE; Recombinant Proteins --metabolism--ME; Sequence Homology, Amino Acid; Substrate Specificity

Molecular Sequence Databank No.: GENBANK/Y12252

CAS Registry No.: 0 (DNA, Recombinant); 0 (Recombinant Proteins)

Enzyme No.: EC 3.5. (Amidohydrolases); EC 3.5.1.4 (amidase)

Record Date Created: 19980129

Record Date Completed: 19980129

2/9/2 (Item 2 from file: 155)

DIALOG(R) File 155:MEDLINE(R)

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12684768 PMID: 7607322

***Pseudomonas aeruginosa* aliphatic amidase is related to the nitrilase/cyanide hydratase enzyme family and Cys166 is predicted to be the active site nucleophile of the catalytic mechanism.**

Novo C; Tata R; Clemente A; Brown P R

Instituto Nacional de Engenharia e Tecnologia Industrial/IBQTA, Queluz, Portugal.

FEBS letters (NETHERLANDS) Jul 3 1995, 367 (3) p275-9, ISSN 0014-5793 Journal Code: 0155157

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

A database search indicated homology between some members of the

nitrilase/cyanide hydratase family, *Pseudomonas aeruginosa* and *Rhodococcus erythropolis* amidases and several other proteins, some of unknown function. BLOCK and PROFILE searches confirmed these relationships and showed that four regions of the *P. aeruginosa* amidase had significant homology with corresponding regions of nitrilases. A phylogenetic tree placed the *P. aeruginosa* and *R. erythropolis* amidases in a group with nitrilases but separated other amidases into three groups. The active site cysteine in nitrilases is conserved in the *P. aeruginosa* amidase indicating that Cys166 is the active site nucleophile.

Tags: Comparative Study; Support, Non-U.S. Gov't

Descriptors: *Amidohydrolases--chemistry--CH; **Pseudomonas aeruginosa* --enzymology--EN; Amidohydrolases--metabolism--ME; Amino Acid Sequence; Aminohydrolases--chemistry--CH; Binding Sites; Cysteine--chemistry--CH; Hydro-Lyases--chemistry--CH; Molecular Sequence Data; Phylogeny; Sequence Alignment; Sequence Homology, Amino Acid

CAS Registry No.: 52-90-4 (Cysteine)

Enzyme No.: EC 3.5. (Amidohydrolases); EC 3.5.1.4 (amidase); EC 3.5.4. (Aminohydrolases); EC 3.5.5.1 (nitrilase); EC 4.2.1. (Hydro-Lyases); EC 4.2.1.66 (cyanide hydratase)

Record Date Created: 19950817

Record Date Completed: 19950817

2/9/7 (Item 7 from file: 155)

DIALOG(R) File 155:MEDLINE(R)

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08977358 PMID: 1907262

Cloning and DNA sequence of *amiC*, a new gene regulating expression of the *Pseudomonas aeruginosa* aliphatic amidase, and purification of the *amiC* product.

Wilson S; Drew R

Department of Biochemistry, University College London, United Kingdom.

Journal of bacteriology (UNITED STATES) Aug 1991, 173 (16) p4914-21,

ISSN 0021-9193 Journal Code: 2985120R

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

Using in vitro-constructed deletions and subcloned DNA fragments, we have identified a new gene, *amiC*, which regulates expression of the inducible *Pseudomonas aeruginosa* aliphatic amidase activity. The DNA sequence of the gene has been determined, and an open reading frame encoding a polypeptide of 385 amino acids (molecular mass, 42,834 Da) has been identified. A search of sequence libraries has failed to find homologies with other published sequences. The *amiC* translation termination codon (A)TGA overlaps the initiation codon for the downstream *amiR* transcription antitermination factor gene, implying that the *amiCR* operon is coordinately regulated. Disruption of the *amiC* open reading frame by insertion and deletion leads to constitutive amidase synthesis, suggesting that *AmiC* is a negative regulator. This is confirmed by the finding that a broad-host-range expression vector carrying *amiC* (pSW41) represses amidase expression in a series of previously characterized *P. aeruginosa* amidase-constitutive mutants. The *AmiC* polypeptide has been purified from PAC452 (pSW41), and N-terminal amino acid sequencing has confirmed the gene identification.

Tags: Support, Non-U.S. Gov't; Support, U.S. Gov't, P.H.S.

Descriptors: *Amidohydrolases--genetics--GE; *Bacterial Proteins --isolation and purification--IP; *Genes, Regulator--genetics--GE; *Periplasmic Binding Proteins; **Pseudomonas aeruginosa*--genetics--GE; *Repressor Proteins--isolation and purification--IP; Amidohydrolases --biosynthesis--BI; Amino Acid Sequence; Bacterial Proteins--genetics--GE; Base Sequence; Enzyme Induction; *Escherichia coli*--metabolism--ME; Gene Expression Regulation, Bacterial; Molecular Sequence Data; Mutation --genetics--GE; Plasmids--genetics--GE; *Pseudomonas aeruginosa*--enzymology --EN; Repressor Proteins--genetics--GE; Restriction Mapping

Molecular Sequence Databank No.: GENBANK/M43175; GENBANK/M74478; GENBANK/M74479; GENBANK/M74480; GENBANK/M74481; GENBANK/M74482; GENBANK/M74483; GENBANK/M74484; GENBANK/S45931; GENBANK/S45975;

GENBANK/X13776

CAS Registry No.: 0 (Bacterial Proteins); 0 (Periplasmic Binding Proteins); 0 (Plasmids); 0 (Repressor Proteins); 142462-53-1 (AmiC protein, *Pseudomonas aeruginosa*)
Enzyme No.: EC 3.5. (Amidohydrolases); EC 3.5.1.4 (amidase)
Record Date Created: 19910905
Record Date Completed: 19910905

2/9/8 (Item 8 from file: 155)

DIALOG(R) File 155:MEDLINE(R)

(c) format only 2004 The Dialog Corp. All rts. reserv.

08102032 PMID: 2495988

Nucleotide sequence of the aliphatic amidase regulator gene (amiR) of *Pseudomonas aeruginosa*.

Lowe N; Rice P M; Drew R E

Department of Biochemistry, University College London, England.

FEBS letters (NETHERLANDS) Mar 27 1989, 246 (1-2) p39-43, ISSN

0014-5793 Journal Code: 0155157

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

The nucleotide sequence of a 1001 bp ClaI/XhoI DNA fragment encoding the amidase regulator gene (amiR) from *Pseudomonas aeruginosa* has been determined. The sequence derives from strain PAC433, a constitutive high expressing amidase mutant, and contains two overlapping open reading frames. Analysis of the sequence has identified one of the reading frames as amiR. The gene encodes a 196 amino acid polypeptide which shows a strong bias towards codons with G or C in the third position. The amiR gene shows no sequence homology with other bacterial regulator proteins.

Tags: Support, Non-U.S. Gov't

Descriptors: *Amidohydrolases--genetics--GE; *Genes, Bacterial; *Genes, Regulator; **Pseudomonas aeruginosa*--genetics--GE; Amino Acid Sequence; Base Sequence; Codon; Deoxyribonucleases, Type II Site-Specific; Molecular Sequence Data; Molecular Weight; *Pseudomonas aeruginosa*--enzymology--EN; Translation, Genetic

Molecular Sequence Databank No.: GENBANK/X13776

CAS Registry No.: 0 (Codon)

Enzyme No.: EC 3.1.21.- (endodeoxyribonuclease ClaI); EC 3.1.21.- (endodeoxyribonuclease XhoI); EC 3.1.21.4 (Deoxyribonucleases, Type II Site-Specific); EC 3.5. (Amidohydrolases); EC 3.5.1.4 (amidase)

Record Date Created: 19890608

Record Date Completed: 19890608

2/9/9 (Item 9 from file: 155)

DIALOG(R) File 155:MEDLINE(R)

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07448694 PMID: 3108029

The amino acid sequence of the aliphatic amidase from *Pseudomonas aeruginosa*.

Ambler R P; Auffret A D; Clarke P H

FEBS letters (NETHERLANDS) May 11 1987, 215 (2) p285-90, ISSN

0014-5793 Journal Code: 0155157

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

Amino acid sequence studies show that the aliphatic amidase (EC 3.5.1.4) from *Pseudomonas aeruginosa* PAC142 consists of a single polypeptide chain of 346 residues, giving an Mr of 38,400. The evidence from the amino acid studies is in complete agreement with that deduced from the DNA sequence of the amiE gene. Studies of the protein from *Pseudomonas putida* A87 show that it differs from the *Ps. aeruginosa* protein by about 30 amino acid

substitutions. It now becomes possible to relate changes in the enzyme which result in altered specificity to structural changes in the protein.

Tags: Support, Non-U.S. Gov't
Descriptors: *Amidohydrolases--analysis--AN; *Pseudomonas aeruginosa
--enzymology--EN; Amino Acid Sequence; Peptide Fragments--analysis--AN
CAS Registry No.: 0 (Peptide Fragments)
Enzyme No.: EC 3.5. (Amidohydrolases); EC 3.5.1.4 (amidase)
Record Date Created: 19870626
Record Date Completed: 19870626

2/9/10 (Item 10 from file: 155)
DIALOG(R) File 155:MEDLINE(R)
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06715270 PMID: 6440948
Complementation analysis of the aliphatic amidase genes of Pseudomonas aeruginosa.

Drew R
Journal of general microbiology (ENGLAND) Dec 1984, 130 (Pt 12)
p3101-11, ISSN 0022-1287 Journal Code: 0375371
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed
Subfile: INDEX MEDICUS

A plasmid, pCL34, capable of autonomous replication in Escherichia coli and Pseudomonas aeruginosa has been constructed which carries the promoter and structural gene (amiE) for P. aeruginosa amidase, but not the regulator gene (amiR). Plasmid pCL34 has been mobilized from E. coli to P. aeruginosa using the broad host range plasmid RP4. Complementation studies were performed in P. aeruginosa strains carrying various amidase mutations. Measurements of amidase activity in the recipients under inducing, non-inducing and repressing conditions showed trans-complementation by the chromosomally located regulator gene product. These results confirmed the positive control model for amidase gene expression. Levels of amidase expression seen during these studies were approximately threefold higher than in the parental, amidase-positive strains.

Tags: Support, Non-U.S. Gov't
Descriptors: *Amidohydrolases--genetics--GE; *Genes, Bacterial; *Genes, Structural; *Pseudomonas aeruginosa--genetics--GE; Chromosome Mapping; Gene Expression Regulation; Genetic Complementation Test; Phenotype; Plasmids; Pseudomonas aeruginosa--enzymology--EN; Transformation, Bacterial
CAS Registry No.: 0 (Plasmids)
Enzyme No.: EC 3.5. (Amidohydrolases)
Record Date Created: 19850314
Record Date Completed: 19850314

2/9/11 (Item 11 from file: 155)
DIALOG(R) File 155:MEDLINE(R)
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05674138 PMID: 6793036
Chloroacetone as an active-site-directed inhibitor of the aliphatic amidase from Pseudomonas aeruginosa.

Hollaway M R; Clarke P H; Ticho T
Biochemical journal (ENGLAND) Dec 1 1980, 191 (3) p811-26, ISSN 0264-6021 Journal Code: 2984726R
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed
Subfile: INDEX MEDICUS

1. Chloroacetone (I) was shown to be an active-site-directed inhibitor of the aliphatic amidase (EC 3.5.1.4) from Pseudomonas aeruginosa strain PAC142.2. This inhibitor reacted with the enzyme in two stages: the first involving the reversible formation of an enzymically inactive species, EI, and the second the formation of a species, EX, from which enzymic activity

could not be recovered. 3. Different types of kinetic experiment were conducted to test conformity of the reaction to the scheme: $E + I \xrightleftharpoons[k-1]{k+1} EI$ Leads to $K+2 \rightarrow EX$ A computer-based analysis of the results was carried out and values of the individual rate constants were determined. 4. No direct evidence for a binding step before the formation of EI could be obtained, as with $[E]_0$ Less Than $[I]_0$ the observed first-order rate constant for the formation of EI was directly proportional to the concentration of chloroacetone up to 1.2 mM (above this concentration the reaction became too rapid to follow even by the stopped-flow method developed to investigate fast inhibition). 5. The value of $k+1$ exhibited a bell-shaped pH-dependency with a maximum value of about $3 \times 10(3) \text{ M}^{-1} \text{ S}^{-1}$ at pH6 and apparent pKa values of 7.8 and about 4.8.6. The values of $k-1$ and $K+2$ were similar and changed with the time of reaction from values of about $3 \times 10(-3) \text{ S}^{-1}$ (pH8.6) at short times to about one-sixth this value for longer periods of incubation. In this respect the simple reaction scheme is insufficient to describe the inhibition process. 7. The overall inhibition reaction is rapid, whether it is considered in relation to the expected chemical reactivity of chloroacetone, the rate of reaction of other enzymes with substrate analogues containing the chloromethyl group, or the rate of the amidase-catalysed hydrolysis of N-methylacetamide, a substrate that is nearly isosteric with chloroacetone. 8. Acetamide protected the amidase from inhibition by chloroacetone, and the concentration-dependence of the protection gave a value of an apparent dissociation constant similar to the K_m value for this substrate. 9. Addition of acetamide to solutions of the species EI led to a slow recovery of activity. Recovery of active enzyme was also observed after dilution of a solution of EI in the absence of substrate. 10. The species EI is considered not to be a simple adsorption complex, and the possibilities are discussed that it may be a tetrahedral carbonyl adduct, a Schiff base (azomethine) or a complex in which the enzyme has undergone a structural change. The species EX is probably a derivative in which there is a covalent bond between a group in the enzyme and the C-1 atom of the inhibitor.

Descriptors: *Acetone--analogs and derivatives--AA; *Amidohydrolases --antagonists and inhibitors--AI; *Pseudomonas aeruginosa--enzymology--EN; Acetamides--pharmacology--PD; Acetone--pharmacology--PD; Binding Sites; Kinetics; Models, Chemical

CAS Registry No.: 0 (Acetamides); 67-64-1 (Acetone); 78-95-5 (chloroacetone)

Enzyme No.: EC 3.5. (Amidohydrolases); EC 3.5.1.4 (amidase)

Record Date Created: 19811119

Record Date Completed: 19811119

2/9/13 (Item 13 from file: 155)

DIALOG(R) File 155:MEDLINE(R)

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05067535 PMID: 110589

Inhibition of the aliphatic amidase from Pseudomonas aeruginosa by urea and related compounds.

Gregoriou M; Brown P R

European journal of biochemistry / FEBS (GERMANY, WEST) May 2 1979, 96

(1) p101-8, ISSN 0014-2956 Journal Code: 0107600

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

The time-dependent inhibition of amidase from Pseudomonas aeruginosa strain AI 3 by urea, hydroxyurea and cyanate displayed saturation kinetics fitting a model for the reaction sequence in which formation of a complex in a reversible step was followed by an irreversible step. Altered amidases from mutant strains AIU 1N and OUCH 4, selected for their resistance to inhibition of growth by urea and hydroxyurea respectively, had altered kinetic constants for inhibition indicating reduced binding capacity for the inhibitors. The substrate acetamide protected AI 3 amidase against inhibition by urea, and altered K_i values for inhibition of the mutant amidases were paralleled by alterations in K_m values for acetamide

indicating that urea acted at the active site. Inhibition of AI 3 amidase involved the binding of one molecule of urea per molecule of enzyme. Urea inhibited amidase slowly regained activity at pH 7.2 through release of urea.

Descriptors: *Amidohydrolases--antagonists and inhibitors--AI; *Pseudomonas aeruginosa--enzymology--EN; *Urea--pharmacology--PD; Cyanates--pharmacology--PD; Enzyme Activation; Hydroxyurea--pharmacology--PD; Kinetics; Molecular Weight

CAS Registry No.: 0 (Cyanates); 127-07-1 (Hydroxyurea); 57-13-6 (Urea)

Enzyme No.: EC 3.5. (Amidohydrolases)

Record Date Created: 19790925

Record Date Completed: 19790925

2/9/14 (Item 14 from file: 155)

DIALOG(R) File 155:MEDLINE(R)

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05063754 PMID: 110350

Kinetic mechanism of the aliphatic amidase from Pseudomonas aeruginosa.

Woods M J; Findlater J D; Orsi B A

Biochimica et biophysica acta (NETHERLANDS) Mar 16 1979, 567 (1) p225-37, ISSN 0006-3002 Journal Code: 0217513

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

The kinetic constants for hydrolysis and transfer (with hydroxylamine as the alternate acceptor) of the aliphatic amidase (acylamide amidohydrolase, EC 3.5.1.4) from Pseudomonas aeruginosa were determined for a variety of acetyl and propionyl derivatives. The results obtained were consistent with a ping-pong or substitution mechanism. Product inhibition, which was pH dependent, implicated an acyl-enzyme compound as a compulsory intermediate and indicated that ammonia combined additionally with the free enzyme in a dead-end manner. The uncompetitive activation of acetamide hydrolysis by hydroxylamine and the observation that the partitioning of products between acetic acid and acetohydroxamate was linearly dependent on the hydroxylamine concentration substantiated these conclusions and indicated that deacylation was at least partially rate limiting. With propionamide as the acyl donor apparently anomalous results, which included inequalities in certain kinetic constants and a hyperbolic dependence of the partition ratio on the hydroxylamine concentration, could be explained by postulating a compulsory isomerisation of the acyl-enzyme intermediate prior to the transfer reaction.

Descriptors: *Amidohydrolases--metabolism--ME; *Pseudomonas aeruginosa--enzymology--EN; Acetamides; Acetic Acids--pharmacology--PD; Acylation; Amides; Amidohydrolases--antagonists and inhibitors--AI; Binding Sites; Hydrolysis; Hydroxylamines--pharmacology--PD; Kinetics; Models, Chemical; Propionates

CAS Registry No.: 0 (Acetamides); 0 (Acetic Acids); 0 (Amides); 0 (Hydroxylamines); 0 (Propionates)

Enzyme No.: EC 3.5. (Amidohydrolases)

Record Date Created: 19790925

Record Date Completed: 19790925

2/9/16 (Item 16 from file: 155)

DIALOG(R) File 155:MEDLINE(R)

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04287097 PMID: 932686

Regulatory properties of an inducible aliphatic amidase in a thermophilic bacillus.

Thalenfeld B; Grossowicz N

Journal of general microbiology (ENGLAND) May 1976, 94 (1) p131-41, ISSN 0022-1287 Journal Code: 0375371

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

A thermophilic bacillus growing on acetamide as both carbon and nitrogen sources produces an inducible amidase. This amidase hydrolysed the following amides in decreasing order of activity, in comparison with acetamide (1.00): propionamide (0.97), fluoroacetamide (0.84), formamide (0.35) and glycine (0.12). Cyanoacetamide, dimethylacetamide, dimethylformamide and urea also induced the synthesis of the amidase, but were not substrates of the enzyme. Studies with protoplasts suggest that the amidase is located in the cytoplasm. Glucose strongly inhibited amidase synthesis; and limiting nitrogen did not release this inhibition. Urea strongly inhibited amidase activity in a competitive manner; but the inhibition caused by iodoacetamide and cyanoacetamide was non-competitive. Both thioacetamide and thiourea were effective inhibitors of enzyme induction. Bacteria grown on a succinate-minimal medium exhibited a lag in amidase synthesis, which could be eliminated by decreasing the concentration of succinate. Acetate- or pyruvate-grown cultures behaved similarly, while those grown on alanine or glutamate exhibited no lag in enzyme induction. In the mutant strain E21, repression of amidase synthesis by glucose was much less evident and no lag for induction was apparent with any of the other carbon sources mentioned.

Descriptors: *Amidohydrolases--biosynthesis--BI; *Bacillus--enzymology--EN; Acetamides--metabolism--ME; Amides--metabolism--ME; Amidohydrolases--metabolism--ME; Bacillus--growth and development--GD; Bacillus--metabolism--ME; Cell-Free System; Cytoplasm--enzymology--EN; Enzyme Induction--drug effects--DE; Enzyme Repression; Glucose--pharmacology--PD; Heat; Kinetics; Protoplasts--enzymology--EN; Thioacetamide--pharmacology--PD; Thiourea--pharmacology--PD; Urea--pharmacology--PD

CAS Registry No.: 0 (Acetamides); 0 (Amides); 50-99-7 (Glucose); 57-13-6 (Urea); 62-55-5 (Thioacetamide); 62-56-6 (Thiourea)

Enzyme No.: EC 3.5. (Amidohydrolases)

Record Date Created: 19760823

Record Date Completed: 19760823

2/9/19 (Item 19 from file: 155)

DIALOG(R) File 155:MEDLINE(R)

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03398192 PMID: 4625925

Biochemical and immunological comparison of aliphatic amidases produced by Pseudomonas species.

Clarke P H

Journal of general microbiology (ENGLAND) Jul 1972, 71 (2) p241-57,
ISSN 0022-1287 Journal Code: 0375371

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

Descriptors: *Amidohydrolases--biosynthesis--BI; *Pseudomonas--enzymology--EN; Acetamides--metabolism--ME; Antigens; Cell-Free System; Cross Reactions; Culture Media; Electrophoresis, Starch Gel; Enzyme Induction; Formamides--metabolism--ME; Genes, Regulator; Genes, Structural; Hydrolases--analysis--AN; Hydrolysis; Immune Sera; Immunodiffusion; Mutation; Phenotype; Pseudomonas--metabolism--ME; Pseudomonas aeruginosa--enzymology--EN; Pseudomonas aeruginosa--immunology--IM; Transferases--analysis--AN

CAS Registry No.: 0 (Acetamides); 0 (Antigens); 0 (Culture Media); 0 (Formamides); 0 (Immune Sera)

Enzyme No.: EC 2. (Transferases); EC 3. (Hydrolases); EC 3.5. (Amidohydrolases)

Record Date Created: 19720922

Record Date Completed: 19720922

2/9/22 (Item 2 from file: 5)

DIALOG(R)File 5:Biosis Previews(R)
(c) 2004 BIOSIS. All rts. reserv.

0011231256 BIOSIS NO.: 199800025503

The aliphatic amidase : Another way to produce ammonia in H. pylori?

AUTHOR: Skouloubris S; Labigne A; De Reuse H

AUTHOR ADDRESS: Inst. Pasteur, Paris, France**France

JOURNAL: Gut 41 (SUPPL. 1): pA14 1997 1997

MEDIUM: print

CONFERENCE/MEETING: European Helicobacter Pylori Study Group Xth
International Workshop on Gastrointestinal Pathology and Helicobacter Pylori
Lisbon, Portugal September 11-14, 1997; 19970911

SPONSOR: European Helicobacter pylori Study Group

ISSN: 0017-5749

DOCUMENT TYPE: Meeting; Meeting Abstract

RECORD TYPE: Citation

LANGUAGE: English

REGISTRY NUMBERS: 7664-41-7: ammonia

DESCRIPTORS:

MAJOR CONCEPTS: Enzymology--Biochemistry and Molecular Biophysics;

Molecular Genetics--Biochemistry and Molecular Biophysics

BIOSYSTEMATIC NAMES: Aerobic Helical or Vibrioid Gram-Negatives--

Eubacteria, Bacteria, Microorganisms

ORGANISMS: Helicobacter-pylori (Aerobic Helical or Vibrioid
Gram-Negatives)

COMMON TAXONOMIC TERMS: Bacteria; Eubacteria; Microorganisms

CHEMICALS & BIOCHEMICALS: aliphatic amidase; ammonia--metabolic
production pathways

MISCELLANEOUS TERMS: Meeting Abstract; Meeting Abstract

CONCEPT CODES:

31500 Genetics of bacteria and viruses

10050 Biochemistry methods - General

10054 Biochemistry methods - Proteins, peptides and amino acids

10808 Enzymes - Physiological studies

13002 Metabolism - General metabolism and metabolic pathways

13012 Metabolism - Proteins, peptides and amino acids

31000 Physiology and biochemistry of bacteria

00520 General biology - Symposia, transactions and proceedings

10060 Biochemistry studies - General

10064 Biochemistry studies - Proteins, peptides and amino acids

36002 Medical and clinical microbiology - Bacteriology

BIOSYSTEMATIC CODES:

06210 Aerobic Helical or Vibrioid Gram-Negatives

2/9/45 (Item 1 from file: 65)

DIALOG(R)File 65:Inside Conferences

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03333046 INSIDE CONFERENCE ITEM ID: CN035225547

Identification of an aliphatic amidase in H. pylori

de Reuse, H.; Skouloubris, S.; Labigne, A.

CONFERENCE: Campylobacter, heliobacter & related organisms--
International workshop; 9th

P: 490

Institute of Child Health, 1998

ISBN: 0620216794

LANGUAGE: English DOCUMENT TYPE: Conference Papers

CONFERENCE EDITOR(S): Lastovica, A. J.; Newell, D. G.; Lastovica, E. E.

CONFERENCE SPONSOR: University of Cape Town

CONFERENCE LOCATION: Cape Town

CONFERENCE DATE: Sep 1997 (199709) (199709)

BRITISH LIBRARY ITEM LOCATION: m00/31914

DESCRIPTORS: campylobacter; heliobacter; organisms; child health

?t s2/3,kwic/36 37 39 40 41 43 44 48

>>>KWIC option is not available in file(s): 399

2/3,KWIC/36 (Item 2 from file: 357)

DIALOG(R)File 357:Derwent Biotech Res.
(c) 2004 Thomson Derwent & ISI. All rts. reserv.

0230013 DBR Accession No.: 99-00114 PATENT
New Helicobacter sp. aliphatic amidase AmiE polypeptides and their encoding sequence - Helicobacter pylori recombinant protein preparation, vector expression in host cell and DNA probe and monoclonal antibody, used for infection diagnosis, recombinant vaccine or therapy
AUTHOR: de Reuse H; Skouloubris S; Labigne A
CORPORATE SOURCE: Paris, France.
PATENT ASSIGNEE: Inst.Pasteur-Paris; INSERM 1998
PATENT NUMBER: WO 9844094 PATENT DATE: 981008 WPI ACCESSION NO.: 98-557106 (9847)
PRIORITY APPLIC. NO.: US 41745 APPLIC. DATE: 970328
NATIONAL APPLIC. NO.: WO 98EP1824 APPLIC. DATE: 980327
LANGUAGE: English

New Helicobacter sp. aliphatic amidase AmiE polypeptides and their encoding sequence

2/3,KWIC/37 (Item 3 from file: 357)
DIALOG(R)File 357:Derwent Biotech Res.
(c) 2004 Thomson Derwent & ISI. All rts. reserv.

0203740 DBR Accession No.: 96-14511
Utilization of acetonitrile and other aliphatic nitriles by a Candida famata strain - acetonitrile degradation using nitrile-hydratase and amidase activity
AUTHOR: Linardi V R; Dias J C T; Rosa C A
CORPORATE AFFILIATE: Univ.Minas-Gerais-Fed.Inst.Biol.Sci.
CORPORATE SOURCE: Departamento de Microbiologia, Instituto de Ciencias Biologicas, Universidade Federal de Minas Gerais, C.P. 486, Belo Horizonte, MG 31270-901, Brazil.
JOURNAL: FEMS Microbiol.Lett. (144, 1, 67-71) 1996
ISSN: 0378-1097 CODEN: FMLED7
LANGUAGE: English

Utilization of acetonitrile and other aliphatic nitriles by a Candida famata strain - acetonitrile degradation using nitrile-hydratase and amidase activity

2/3,KWIC/39 (Item 1 from file: 340)
DIALOG(R)File 340:CLAIMS(R)/US Patent
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3528971 0122998
C/HELICOBACTER ALIPHATIC AMIDASE AMIE POLYPEPTIDES, AND DNA SEQUENCES ENCODING THOSE POLYPEPTIDES; SCREENING BY CONTACTING ENZYME WITH COMPOUND, AND SELECTING COMPOUND WHICH INHIBITS ENZYME ACTIVITY; ANTIULCER AGENTS; BACTERICIDES
Inventors: De Reuse Hilde (FR); Labigne Agnes (FR); Skouloubris Stephane (FR)
Assignee: Institut Pasteur FR
Assignee Code: 42312

	Kind	Publication Number	Date	Application Number	Date
Priority Applic:	B	US 6248551	20010619	US 9827900	19980223
Provisional Applic:				US 9827900	19980223
Calculated Expiration:				US 60-41745	19970328

HELICOBACTER ALIPHATIC AMIDASE AMIE POLYPEPTIDES, AND DNA SEQUENCES ENCODING THOSE POLYPEPTIDES...

2/3,KWIC/40 (Item 2 from file: 340)
DIALOG(R)File 340:CLAIMS(R)/US Patent
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3168988 9921350

**C/PREPARATION OF LACTAMS FROM ALIPHATIC ALPHA, OMEGA-DINITILES; ISOLATED
COMAMONAS TESTOSTERONI 5-MGAM-4D WITH NITRILE HYDRATASE AND AMIDASE
ACTIVITIES; FOR HIGH YIELD WITH HIGH REGIOSELECTIVITY AND BY PRODUCT
INHIBITION**

Inventors: Di Cosimo Robert (US); Fallon Robert Donald (US); Gavagan John
Edward (US); Herkes Frank Edward (US)

Assignee: Du Pont de Nemours, E I & Co

Assignee Code: 25048

	Kind	Publication Number	Date	Application Number	Date
	A	US 5922589	19990713	US 98108729	19980701
Division of:		US 5858736		US 96650073	19960517
Priority Applic:				US 98108729	19980701
				US 96650073	19960517

Calculated Expiration: 20160517

**PREPARATION OF LACTAMS FROM ALIPHATIC ALPHA, OMEGA-DINITILES...
...ISOLATED COMAMONAS TESTOSTERONI 5-MGAM-4D WITH NITRILE HYDRATASE AND
AMIDASE ACTIVITIES; FOR HIGH YIELD WITH HIGH REGIOSELECTIVITY AND BY
PRODUCT INHIBITION**

2/3,KWIC/41 (Item 3 from file: 340)
DIALOG(R)File 340:CLAIMS(R)/US Patent
(c) 2004 IFI/CLAIMS(R). All rts. reserv.

3096789 9901716

**C/PREPARATION OF LACTAMS FROM ALIPHATIC ALPHA, OMEGA-DINITRILES;
CONTACTING DINITRILE IN AQUEOUS MIXTURE WITH ENZYME CATALYST HAVING
ALIPHATIC NITRILASE ACTIVITY OR COMBINATION OF NITRILE HYDRATASE AND
AMIDASE ACTIVITY, CONTACTING PRODUCT WITH HYDROGEN AND HYDROGENATION
CATALYST TO PRODUCE LACTAM**

Inventors: Di Cosimo Robert (US); Fallon Robert Donald (US); Gavagan John
Edward (US); Herkes Frank Edward (US)

Assignee: Du Pont de Nemours, E I & Co

Assignee Code: 25048

	Kind	Publication Number	Date	Application Number	Date
	A	US 5858736	19990112	US 96650073	19960517
Priority Applic:				US 96650073	19960517

Calculated Expiration: 20160517

CERTIFICATE OF CORRECTION: 19990928

**PREPARATION OF LACTAMS FROM ALIPHATIC ALPHA, OMEGA-DINITRILES...
...CONTACTING DINITRILE IN AQUEOUS MIXTURE WITH ENZYME CATALYST HAVING
ALIPHATIC NITRILASE ACTIVITY OR COMBINATION OF NITRILE HYDRATASE AND
AMIDASE ACTIVITY, CONTACTING PRODUCT WITH HYDROGEN AND HYDROGENATION
CATALYST TO PRODUCE LACTAM**

2/3,KWIC/43 (Item 2 from file: 654)
DIALOG(R)File 654:US Pat.Full.
(c) Format only 2004 The Dialog Corp. All rts. reserv.

4166734

Derwent Accession: 1998-041747

Utility

**C/ Preparation of lactams from aliphatic [alpha],[omega]-Dinitiles
; ISOLATED COMAMONAS TESTOSTERONI 5-MGAM-4D WITH NITRILE HYDRATASE AND
AMIDASE ACTIVITIES; FOR HIGH YIELD WITH HIGH REGIOSELECTIVITY AND BY
PRODUCT INHIBITION**

Inventor: Di Cosimo, Robert, Rockland, DE
Fallon, Robert Donald, Elkton, MD
Gavagan, John Edward, Wilmington, DE
Herkes, Frank Edward, Wilmington, DE
Assignee: E. I. du Pont de Nemours and Company (02), Wilmington, DE
Du Pont de Nemours, E I & Co (Code: 25048)
Examiner: Lilling, Herbert J. (Art Unit: 161)

	Publication Number	Kind	Date	Application Number	Filing Date
Main Patent	US 5922589	A	19990713	US 98108729	19980701
Division	US 5858736	A	19990112	US 96650073	19960517

Fulltext Word Count: 19383

Preparation of lactams from aliphatic [alpha],[omega]-Dinitiles

2/3,KWIC/44 (Item 3 from file: 654)
DIALOG(R)File 654:US Pat.Full.
(c) Format only 2004 The Dialog Corp. All rts. reserv.

4095232
Derwent Accession: 1998-041747

Utility

CERTIFICATE OF CORRECTION

**C/ Preparation of lactams from aliphatic [alpha],[omega]-dinitriles
; CONTACTIN G DINITRILE IN AQUEOUS MIXTURE WITH ENZYME CATALYST HAVING
ALIPHATIC NITRILASE ACTIVITY OR COMBINATION OF NITRILE HYDRATASE AND
AMIDASE ACTIVITY, CONTACTING PRODUCT WITH HYDROGEN AND HYDROGENATION
CATALYST TO PRODUCE LACTAM**

Inventor: Di Cosimo, Robert, Rockland, DE
Fallon, Robert Donald, Elkton, MD
Gavagan, John Edward, Wilmington, DE
Herkes, Frank Edward, Wilmington, DE
Assignee: E. I. du Pont de Nemours and Company (02), Wilmington, DE
Du Pont de Nemours, E I & Co (Code: 25048)
Examiner: Lilling, Herbert J. (Art Unit: 161)

	Publication Number	Kind	Date	Application Number	Filing Date
Main Patent	US 5858736	A	19990112	US 96650073	19960517

Fulltext Word Count: 20552

Preparation of lactams from aliphatic [alpha],[omega]-dinitriles

2/3,KWIC/48 (Item 1 from file: 349)
DIALOG(R)File 349:PCT FULLTEXT
(c) 2004 WIPO/Univentio. All rts. reserv.

00453630

**i(HELICOBACTER) ALIPHATIC AMIDASE POLYPEPTIDES, DNA SEQUENCES ENCODING
THOSE POLYPEPTIDES AND USES THEREOF
POLYPEPTIDES DE L' AMIDASE ALIPHATIQUE Amie D'i(HELICOBACTER)ET SEQUENCES
D'ADN CODANT LESDITS POLYPEPTIDES**

Patent Applicant/Assignee:
INSTITUT PASTEUR,
INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE,
DE REUSE Hilde,
SKOULOUBRIS Stephane,

LABIGNE Agnes,
 Inventor(s):
 DE REUSE Hilde,
 SKOULOUBRIS Stephane,
 LABIGNE Agnes,
 Patent and Priority Information (Country, Number, Date):
 Patent: WO 9844094 A2 19981008
 Application: WO 98EP1824 19980327 (PCT/WO EP9801824)
 Priority Application: US 9741745 19970328
 Designated States: AL AM AT AU AZ BA BB BG BR BY CA CH CN CU CZ DE DK EE ES
 FI GB GE GH GM GW HU IL IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MD MG
 MK MN MW MX NO NZ PL PT RO RU SD SE SG SI SK SL TJ TM TR TT UA UG US UZ
 VN YU ZW GH GM KE LS MW SD SZ UG ZW AM AZ BY KG KZ MD RU TJ TM AT BE CH
 DE DK ES FI FR GB GR IE IT LU MC NL PT SE BF BJ CF CG CI CM GA GN ML MR
 NE SN TD TG
 Publication Language: English
 Fulltext Word Count: 9017

i(HELICOBACTER) ALIPHATIC AMIDASE POLYPEPTIDES, DNA SEQUENCES ENCODING
 THOSE POLYPEPTIDES AND USES THEREOF
 POLYPEPTIDES DE L' AMIDASE ALIPHATIQUE Amie D'i(HELICOBACTER) ET SEQUENCES
 D'ADN CODANT LESDITS POLYPEPTIDES
 ?logoff hold

13apr04 12:19:15 User228206 Session D2146.7
 \$0.48 0.150 DialUnits File155
 \$2.31 11 Type(s) in Format 9
 \$2.31 11 Types
 \$2.79 Estimated cost File155
 \$0.13 0.023 DialUnits File5
 \$1.75 1 Type(s) in Format 9
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 \$1.88 Estimated cost File5
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 \$1.60 1 Types

\$1.76 Estimated cost File349
OneSearch, 16 files, 0.577 DialUnits FileOS
\$0.24 TELNET
\$22.06 Estimated cost this search
\$22.06 Estimated total session cost 0.577 DialUnits

Status: Signed Off. (1 minutes)

\$0.04 Estimated cost File467
 OneSearch, 26 files, 0.162 DialUnits FileOS
 \$0.02 TELNET
 \$1.03 Estimated cost this search
 \$1.03 Estimated total session cost 0.162 DialUnits

File 155:MEDLINE(R) 1966-2004/Apr W1

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***File 155: Medline has been reloaded. Accession numbers**
 have changed. Please see HELP NEWS 154 for details.

Set	Items	Description
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?s aliphatic?	(3n)	amidase?
	6440	ALIPHATIC?
	2018	AMIDASE?
S1	42	ALIPHATIC? (3N) AMIDASE?
?s s1/1998:2004		
	42	S1
	3111437	PY=1998 : PY=2004
S2	12	S1/1998:2004
?s s1 not s2		
	42	S1
	12	S2
S3	30	S1 NOT S2
?t s3/9/all		

3/9/1

DIALOG(R)File 155:MEDLINE(R)

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13675690 PMID: 9364923

Identification and characterization of an aliphatic amidase in Helicobacter pylori.

Skouloubris S; Labigne A; De Reuse H
 Unite de Pathogenie Bacterienne des Muqueuses, Institut Pasteur, Paris, France.

Molecular microbiology (ENGLAND) Sep 1997, 25 (5) p989-98, ISSN 0950-382X Journal Code: 8712028

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

We report, for the first time, the presence in *Helicobacter pylori* of an **aliphatic amidase** that, like urease, contributes to ammonia production. **Aliphatic amidases** are cytoplasmic acylamide amidohydrolases (EC 3.5.1.4) hydrolysing short-chain aliphatic amides to produce ammonia and the corresponding organic acid. The finding of an **aliphatic amidase** in *H. pylori* was unexpected as this enzyme has only previously been described in bacteria of environmental (soil or water) origin. The *H. pylori* amidase gene *amiE* (1017 bp) was sequenced, and the deduced amino acid sequence of *AmiE* (37746Da) is very similar (75% identity) to the other two sequenced **aliphatic amidases**, one from *Pseudomonas aeruginosa* and one from *Rhodococcus* sp. R312. Amidase activity was measured as the release of ammonia by sonicated crude extracts from *H. pylori* strains and from recombinant *Escherichia coli* strains overproducing the *H. pylori* amidase. The substrate specificity was analysed with crude extracts from *H. pylori* cells grown in vitro; the best substrates were propionamide, acrylamide and acetamide. Polymerase chain reaction (PCR) amplification of an internal *amiE* sequence was obtained with each of 45 different *H. pylori* clinical isolates, suggesting that amidase is common to all *H. pylori* strains. A *H. pylori* mutant (N6-836) carrying an interrupted *amiE* gene was constructed by allelic exchange. No amidase activity could be detected in N6-836. In a N6-urease negative mutant, amidase activity was two- to threefold higher than in the parental strain N6. Crude extracts of strain N6 slowly hydrolysed formamide. This activity was affected in neither the amidase negative strain (N6-836) nor a double mutant strain deficient in both

amidase and urease activities, suggesting the presence of an independent discrete formamidase in *H. pylori*. The existence of an **aliphatic amidase**, a correlation between the urease and amidase activities and the possible presence of a formamidase indicates that *H. pylori* has a large range of possibilities for intracellular ammonia production.

Tags: Comparative Study; Support, Non-U.S. Gov't

Descriptors: *Amidohydrolases--analysis--AN; *Helicobacter pylori--enzymology--EN; Amino Acid Sequence; Cloning, Molecular; DNA, Recombinant; Escherichia coli--enzymology--EN; Escherichia coli--genetics--GE; Genes, Structural, Bacterial--genetics--GE; Helicobacter pylori--chemistry--CH; Helicobacter pylori--genetics--GE; Molecular Sequence Data; Mutation--genetics--GE; Recombinant Proteins--genetics--GE; Recombinant Proteins--metabolism--ME; Sequence Homology, Amino Acid; Substrate Specificity

Molecular Sequence Databank No.: GENBANK/Y12252

CAS Registry No.: 0 (DNA, Recombinant); 0 (Recombinant Proteins)

Enzyme No.: EC 3.5. (Amidohydrolases); EC 3.5.1.4 (amidase)

Record Date Created: 19980129

Record Date Completed: 19980129

3/9/2

DIALOG(R) File 155:MEDLINE(R)

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13022578 PMID: 8662959

A novel gene cluster including the Rhodococcus rhodochrous J1 nhlBA genes encoding a low molecular mass nitrile hydratase (L-NHase) induced by its reaction product.

Komeda H; Kobayashi M; Shimizu S

Department of Agricultural Chemistry, Faculty of Agriculture, Kyoto University, Kyoto 606-01, Japan.

Journal of biological chemistry (UNITED STATES) Jun 28 1996, 271 (26) p15796-802, ISSN 0021-9258 Journal Code: 2985121R

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

The 3.5 kilobases (kb) of the 5'-upstream region from nhlBA encoding a cobalt-containing low molecular mass nitrile hydratase (L-NHase) from *Rhodococcus rhodochrous* J1 was found to be required for the amide-dependent expression of nhlBA in experiments using a *Rhodococcus* transformation system. Sequence analysis of the 3.5-kb fragment revealed the presence of two open reading frames (nhlD and nhlC) in this fragment. NhlD has similarity to regulators MerR, CadC, and ArsR. NhlC has similarity to the regulators AmiC, for the expression of an **aliphatic amidase** from *Pseudomonas aeruginosa*, and NhhC, for the expression of a high molecular mass nitrile hydratase from *R. rhodochrous* J1. Assays of NHase activity of transformants carrying nhlD deletion or nhlC deletion mutations suggest a negative regulatory role for nhlD and a positive regulatory role for nhlC in the process of the L-NHase formation. Assays of NHase and amidase activities and Western blot analyses of each *Rhodococcus* transformant carrying various deletion plasmids, have shown that nhlBA and amdA encoding an amidase, which is located 1.9 kb downstream of nhlBA, were regulated in the same manner. These findings present the genetic evidence for a novel gene cluster controlling the expression of L-NHase, which is induced by the reaction product (amide) in the "practical microorganism" *R. rhodochrous* J1.

Tags: Comparative Study; Support, Non-U.S. Gov't

Descriptors: *Gene Expression Regulation, Bacterial; *Genes, Structural, Bacterial; *Hydro-Lyases--genetics--GE; *Nitriles--metabolism--ME; *Rhodococcus--genetics--GE; Base Sequence; Cloning, Molecular; DNA, Bacterial--genetics--GE; Gene Expression Regulation, Bacterial--drug effects--DE; Gene Expression Regulation, Enzymologic--drug effects--DE; Molecular Sequence Data; Molecular Weight; Open Reading Frames; RNA, Messenger--genetics--GE; Restriction Mapping; Sequence Alignment; Sequence Homology, Amino Acid

Molecular Sequence Databank No.: GENBANK/D67028

CAS Registry No.: 0 (DNA, Bacterial); 0 (Nitriles); 0 (RNA,

Messenger)

Enzyme No.: EC 4.2.1. (Hydro-Lyases); EC 4.2.1.- (nitrile hydratase)

Record Date Created: 19960820

Record Date Completed: 19960820

3/9/3

DIALOG(R) File 155:MEDLINE(R)

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12684768 PMID: 7607322

Pseudomonas aeruginosa aliphatic amidase is related to the nitrilase/cyanide hydratase enzyme family and Cys166 is predicted to be the active site nucleophile of the catalytic mechanism.

Novo C; Tata R; Clemente A; Brown P R

Instituto Nacional de Engenharia e Tecnologia Industrial/IBQTA, Queluz, Portugal.

FEBS letters (NETHERLANDS) Jul 3 1995, 367 (3) p275-9, ISSN 0014-5793 Journal Code: 0155157

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

A database search indicated homology between some members of the nitrilase/cyanide hydratase family, *Pseudomonas aeruginosa* and *Rhodococcus erythropolis* amidases and several other proteins, some of unknown function. BLOCK and PROFILE searches confirmed these relationships and showed that four regions of the *P. aeruginosa* amidase had significant homology with corresponding regions of nitrilases. A phylogenetic tree placed the *P. aeruginosa* and *R. erythropolis* amidases in a group with nitrilases but separated other amidases into three groups. The active site cysteine in nitrilases is conserved in the *P. aeruginosa* amidase indicating that Cys166 is the active site nucleophile.

Tags: Comparative Study; Support, Non-U.S. Gov't

Descriptors: *Amidohydrolases--chemistry--CH; **Pseudomonas aeruginosa* --enzymology--EN; Amidohydrolases--metabolism--ME; Amino Acid Sequence; Aminoalcohols--chemistry--CH; Binding Sites; Cysteine--chemistry--CH; Hydro-Lyases--chemistry--CH; Molecular Sequence Data; Phylogeny; Sequence Alignment; Sequence Homology, Amino Acid

CAS Registry No.: 52-90-4 (Cysteine)

Enzyme No.: EC 3.5. (Amidohydrolases); EC 3.5.1.4 (amidase); EC 3.5.4. (Aminohydrolases); EC 3.5.5.1 (nitrilase); EC 4.2.1. (Hydro-Lyases); EC 4.2.1.66 (cyanide hydratase)

Record Date Created: 19950817

Record Date Completed: 19950817

3/9/4

DIALOG(R) File 155:MEDLINE(R)

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10289814 PMID: 7987228

A new family of carbon-nitrogen hydrolases.

Bork P; Koonin E V

European Molecular Biology Laboratory, Heidelberg, Germany.

Protein science - a publication of the Protein Society (UNITED STATES)

Aug 1994, 3 (8) p1344-6, ISSN 0961-8368 Journal Code: 9211750

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

Using computer methods for database search and multiple alignment, statistically significant sequence similarities were identified between several nitrilases with distinct substrate specificity, cyanide hydratases, **aliphatic amidases**, beta-alanine synthase, and a few other proteins with unknown molecular function. All these proteins appear to be involved in the reduction of organic nitrogen compounds and ammonia production.

Sequence conservation over the entire length, as well as the similarity in the reactions catalyzed by the known enzymes in this family, points to a common catalytic mechanism. The new family of enzymes is characterized by several conserved motifs, one of which contains an invariant cysteine that is part of the catalytic site in nitrilases. Another highly conserved motif includes an invariant glutamic acid that might also be involved in catalysis.

Tags: Comparative Study

Descriptors: *Hydrolases--chemistry--CH; *Sequence Alignment; Amidohydrolases--chemistry--CH; Amidohydrolases--metabolism--ME; Amino Acid Sequence; Aminohydrolases--chemistry--CH; Aminohydrolases--metabolism--ME; Ammonia--pharmacology--PD; Databases, Factual; Hydro-Lyases--chemistry--CH; Hydro-Lyases--metabolism--ME; Hydrolases--metabolism--ME; Information Storage and Retrieval; Molecular Sequence Data; Open Reading Frames; Sequence Homology

Molecular Sequence Databank No.: GENBANK/X52543; GENBANK/X66132; GENBANK/Z14933

CAS Registry No.: 7664-41-7 (Ammonia)

Enzyme No.: EC 3. (Hydrolases); EC 3.5. (Amidohydrolases); EC 3.5.1.6 (beta-ureidopropionase); EC 3.5.4. (Aminohydrolases); EC 3.5.5.1 (nitrilase); EC 4.2.1. (Hydro-Lyases); EC 4.2.1.66 (cyanide hydratase)

Record Date Created: 19950111

Record Date Completed: 19950111

3/9/5

DIALOG(R) File 155: MEDLINE(R)

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10242343 PMID: 7944367

Purification and characterization of an amidase from an acrylamide-degrading Rhodococcus sp.

Nawaz M S; Khan A A; Seng J E; Leakey J E; Siitonen P H; Cerniglia C E
Division of Microbiology, National Center for Toxicological Research,
Food and Drug Administration, Jefferson, Arkansas 72079.

Applied and environmental microbiology (UNITED STATES) Sep 1994, 60
(9) p3343-8, ISSN 0099-2240 Journal Code: 7605801

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

A constitutively expressed **aliphatic amidase** from a *Rhodococcus* sp. catalyzing acrylamide deamination was purified to electrophoretic homogeneity. The molecular weight of the native enzyme was estimated to be 360,000. Upon sodium dodecyl sulfate-polyacrylamide gel electrophoresis, the purified preparation yielded a homogeneous protein band having an apparent molecular weight of about 44,500. The amidase had pH and temperature optima of 8.5 and 40 degrees C, respectively, and its isoelectric point was pH 4.0. The amidase had apparent K_m values of 1.2, 2.6, 3.0, 2.7, and 5.0 mM for acrylamide, acetamide, butyramide, propionamide, and isobutyramide, respectively. Inductively coupled plasma-atomic emission spectrometry analysis indicated that the enzyme contains 8 mol of iron per mol of the native enzyme. No labile sulfide was detected. The amidase activity was enhanced by, but not dependent on $Fe(2+)$, $Ba(2+)$, and $Cr(2+)$. However, the enzyme activity was partially inhibited by $Mg(2+)$ and totally inhibited in the presence of $Ni(2+)$, $Hg(2+)$, $Cu(2+)$, $Co(2+)$, specific iron chelators, and thiol blocking reagents. The NH_2 -terminal sequence of the first 18 amino acids displayed 88% homology to the **aliphatic amidase** of *Brevibacterium* sp. strain R312.

Descriptors: *Acrylamides--metabolism--ME; *Amidohydrolases--isolation and purification--IP; *Rhodococcus--metabolism--ME; Acrylamide; Amidohydrolases--chemistry--CH; Amidohydrolases--genetics--GE; Amino Acid Sequence; Amino Acids--analysis--AN; Biodegradation; Isoelectric Point; Kinetics; Metals--pharmacology--PD; Molecular Sequence Data; Molecular Weight; Rhodococcus--genetics--GE; Rhodococcus--isolation and purification--IP; Substrate Specificity; Temperature

CAS Registry No.: 0 (Acrylamides); 0 (Amino Acids); 0 (Metals);

79-06-1 (Acrylamide)

Enzyme No.: EC 3.5. (Amidohydrolases); EC 3.5.1.4 (amidase)

Record Date Created: 19941118

Record Date Completed: 19941118

3/9/6

DIALOG(R) File 155:MEDLINE(R)

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10160827 PMID: 8051020

Identification and structure of the nasR gene encoding a nitrate- and nitrite-responsive positive regulator of nasFEDCBA (nitrate assimilation) operon expression in Klebsiella pneumoniae M5a1.

Goldman B S; Lin J T; Stewart V

Sections of Microbiology, Cornell University, Ithaca, New York 14853-8101.

Journal of bacteriology (UNITED STATES) Aug 1994, 176 (16) p5077-85, ISSN 0021-9193 Journal Code: 2985120R

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

Klebsiella pneumoniae can use nitrate and nitrite as sole nitrogen sources through the nitrate assimilatory pathway. The structural genes for assimilatory nitrate and nitrite reductases together with genes necessary for nitrate transport form an operon, nasFEDCBA. Expression of the nasF operon is regulated both by general nitrogen control and also by nitrate or nitrite induction. We have identified a gene, nasR, that is necessary for nitrate and nitrite induction. The nasR gene, located immediately upstream of the nasFEDCBA operon, encodes a 44-kDa protein. The NasR protein shares carboxyl-terminal sequence similarity with the AmiR protein of Pseudomonas aeruginosa, the positive regulator of amiE (**aliphatic amidase**) gene expression. In addition, we present evidence that the nasF operon is not autogenously regulated.

Tags: Support, U.S. Gov't, Non-P.H.S.

Descriptors: *Gene Expression Regulation, Bacterial; *Genes, Regulator; *Genes, Structural, Bacterial; *Klebsiella pneumoniae--genetics--GE; *Nitrates--metabolism--ME; *Nitrites--metabolism--ME; *Trans-Activators--genetics--GE; Amino Acid Sequence; Base Sequence; DNA-Binding Proteins--metabolism--ME; Molecular Sequence Data; Mutagenesis, Insertional; Operon; Trans-Activation (Genetics)

Molecular Sequence Databank No.: GENBANK/L27824

CAS Registry No.: 0 (DNA-Binding Proteins); 0 (Nitrates); 0 (Nitrites); 0 (Trans-Activators); 0 (nasR protein)

Gene Symbol: amiR; nadB; nasA; nasC; nasD; nasE; nasF; nasR

Record Date Created: 19940907

Record Date Completed: 19940907

3/9/7

DIALOG(R) File 155:MEDLINE(R)

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09908517 PMID: 8253087

Antitermination of amidase expression in Pseudomonas aeruginosa is controlled by a novel cytoplasmic amide-binding protein.

Wilson S A; Wachira S J; Drew R E; Jones D; Pearl L H

Biomolecular Structure Group, University College London, UK.

EMBO journal (ENGLAND) Sep 1993, 12 (9) p3637-42, ISSN 0261-4189
Journal Code: 8208664

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

Amide-inducible expression of the **aliphatic amidase** system of Pseudomonas aeruginosa can be reconstituted in Escherichia coli with only

the amidase structural gene *amiE*, the negative regulator *amiC* and the positive regulator *amiR*, a transcription antitermination factor. Complementation experiments in *E. coli* suggest that negative control of amidase expression by *AmiC* is mediated by a protein-protein interaction with *AmiR*. Purified *AmiC* binds acetamide with a *KD* of 3.7 μM in equilibrium dialysis studies, and therefore *AmiC* appears to be the sensory partner of the *AmiC/AmiR* pair of regulatory proteins, responding to the presence of amides. Sequence analysis techniques suggest that *AmiC* is a member of the structural family of periplasmic binding proteins, but has a distinct and novel cytoplasmic role.

Tags: Comparative Study; Support, Non-U.S. Gov't

Descriptors: *Amidohydrolases--biosynthesis--BI; *Bacterial Proteins--metabolism--ME; *Gene Expression Regulation, Bacterial; *Gene Expression Regulation, Enzymologic; *Genes, Bacterial; *Periplasmic Binding Proteins; *Pseudomonas aeruginosa--enzymology--EN; *Repressor Proteins--metabolism--ME; Amidohydrolases--genetics--GE; Amino Acid Sequence; Bacterial Proteins--biosynthesis--BI; Consensus Sequence; Genes, Regulator; Genes, Structural, Bacterial; Genetic Complementation Test; Kinetics; Molecular Sequence Data; Operon; Protein Structure, Secondary; Pseudomonas aeruginosa--metabolism--ME; Restriction Mapping; Sequence Homology, Amino Acid

CAS Registry No.: 0 (Bacterial Proteins); 0 (Periplasmic Binding Proteins); 0 (Repressor Proteins); 142462-53-1 (*AmiC* protein, *Pseudomonas aeruginosa*)

Enzyme No.: EC 3.5. (Amidohydrolases); EC 3.5.1.4 (amidase)

Gene Symbol: *amiB*; *amiC*; *amiE*; *amiR*; *amiS*

Record Date Created: 19940110

Record Date Completed: 19940110

3/9/8

DIALOG(R) File 155:MEDLINE(R)

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09774423 PMID: 8336670

Structural, functional, and evolutionary relationships among extracellular solute-binding receptors of bacteria.

Tam R; Saier M H

Department of Biology, University of California, San Diego, La Jolla 92093-0116.

Microbiological reviews (UNITED STATES) Jun 1993, 57 (2) p320-46,

ISSN 0146-0749 Journal Code: 7806086

Contract/Grant No.: 2R01AI14176; AI; NIAID; 5R01AI21702; AI; NIAID

Document type: Journal Article; Review; Review, Academic

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

Extracellular solute-binding proteins of bacteria serve as chemoreceptors, recognition constituents of transport systems, and initiators of signal transduction pathways. Over 50 sequenced periplasmic solute-binding proteins of gram-negative bacteria and homologous extracytoplasmic lipoproteins of gram-positive bacteria have been analyzed for sequence similarities, and their degrees of relatedness have been determined. Some of these proteins are homologous to cytoplasmic transcriptional regulatory proteins of bacteria; however, with the sole exception of the vitamin B12-binding protein of *Escherichia coli*, which is homologous to human glutathione peroxidase, they are not demonstrably homologous to any of the several thousand sequenced eukaryotic proteins. Most of these proteins fall into eight distinct clusters as follows. Cluster 1 solute-binding proteins are specific for malto-oligosaccharides, multiple oligosaccharides, glycerol 3-phosphate, and iron. Cluster 2 proteins are specific for galactose, ribose, arabinose, and multiple monosaccharides, and they are homologous to a number of transcriptional regulatory proteins including the lactose, galactose, and fructose repressors of *E. coli*. Cluster 3 proteins are specific for histidine, lysine-arginine-ornithine, glutamine, octopine, nopaline, and basic amino acids. Cluster 4 proteins are specific for leucine and leucine-isoleucine-valine, and they are homologous to the **aliphatic amidase** transcriptional repressor, *AmiC*, of *Pseudomonas aeruginosa*.

Cluster 5 proteins are specific for dipeptides and oligopeptides as well as nickel. Cluster 6 proteins are specific for sulfate, thiosulfate, and possibly phosphate. Cluster 7 proteins are specific for dicarboxylates and tricarboxylates, but these two proteins exhibit insufficient sequence similarity to establish homology. Finally, cluster 8 proteins are specific for iron complexes and possibly vitamin B12. Members of each cluster of binding proteins exhibit greater sequence conservation in their N-terminal domains than in their C-terminal domains. Signature sequences for these eight protein families are presented. The results reveal that binding proteins specific for the same solute from different bacteria are generally more closely related to each other than are binding proteins specific for different solutes from the same organism, although exceptions exist. They also suggest that a requirement for high-affinity solute binding imposes severe structural constraints on a protein. The occurrence of two distinct classes of bacterial cytoplasmic repressor proteins which are homologous to two different clusters of periplasmic binding proteins suggests that the gene-splicing events which allowed functional conversion of these proteins with retention of domain structure have occurred repeatedly during evolutionary history. (ABSTRACT TRUNCATED AT 400 WORDS) (227 Refs.)

Tags: Support, U.S. Gov't, P.H.S.

Descriptors: *Bacteria--metabolism--ME; *Bacterial Proteins--analysis--AN; *Carrier Proteins--analysis--AN; Amino Acid Sequence; Bacterial Proteins--chemistry--CH; Biological Transport; Carrier Proteins--chemistry--CH; Carrier Proteins--physiology--PH; Evolution; Molecular Sequence Data; Structure-Activity Relationship

CAS Registry No.: 0 (Bacterial Proteins); 0 (Carrier Proteins)

Record Date Created: 19930824

Record Date Completed: 19930824

3/9/9

DIALOG(R) File 155:MEDLINE(R)

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09368661 PMID: 1628849

Cloning and primary structure of the wide-spectrum amidase from *Brevibacterium* sp. R312: high homology to the *amiE* product from *Pseudomonas aeruginosa*.

Soubrier F; Levy-Schil S; Mayaux J F; Petre D; Arnaud A; Crouzet J

Departement Biotechnologie, Rhone-Poulenc Rorer, Centre de Recherche de Vitry-Alfortville, Vitry sur Seine, France.

Gene (NETHERLANDS) Jul 1 1992, 116 (1) p99-104, ISSN 0378-1119

Journal Code: 7706761

Erratum in Gene 1993 Feb 28;124(2) 309

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

A *Brevibacterium* sp. R312 DNA fragment encoding the wide-spectrum amidase (EC 3.5.1.4) has been cloned and sequenced, using limited amino acid (aa) sequence information obtained from the purified enzyme. The deduced aa sequence showed more than 80% strict identity with the *Pseudomonas aeruginosa* **aliphatic amidase**, the product of the *amiE* gene, suggesting a horizontal transfer of the gene during evolution between Gram+ and Gram-bacteria.

Descriptors: *Amidohydrolases--genetics--GE; **Brevibacterium*--enzymology--EN; **Escherichia coli*--genetics--GE; **Pseudomonas aeruginosa*--enzymology--EN; Amidohydrolases--chemistry--CH; Amidohydrolases--metabolism--ME; Amino Acid Sequence; Base Sequence; *Brevibacterium*--genetics--GE; Cloning, Molecular; *Escherichia coli*--enzymology--EN; Molecular Sequence Data; *Pseudomonas aeruginosa*--genetics--GE; Recombinant Proteins--genetics--GE; Recombinant Proteins--metabolism--ME; Restriction Mapping

Molecular Sequence Databank No.: GENBANK/M74890; GENBANK/M74891; GENBANK/M74892; GENBANK/M76451; GENBANK/M77131; GENBANK/M77132; GENBANK/M79309; GENBANK/M79310; GENBANK/S38798; GENBANK/S38799

CAS Registry No.: 0 (Recombinant Proteins)

Enzyme No.: EC 3.5. (Amidohydrolases); EC 3.5.1.4 (amidase)

Gene Symbol: *amiE*

Record Date Created: 19920817
Record Date Completed: 19920817

3/9/10

DIALOG(R) File 155:MEDLINE(R)

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09284651 PMID: 1368108

N-terminal amino acid sequence of Brevibacterium sp. R312 wide-spectrum amidase.

Chion C K; Duran R; Arnaud A; Galzy P
Chaire de Microbiologie Industrielle et de Genetique des Microorganismes,
Ecole Nationale Supérieure Agronomique de Montpellier, France.

Applied microbiology and biotechnology (GERMANY) Nov 1991, 36 (2)
p205-7, ISSN 0175-7598 Journal Code: 8406612

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: BIOTECHNOLOGY

A wide-spectrum amidase from Brevibacterium sp. R312 was partially purified. The enzyme subunit was purified by reversed phase HPLC and the N-terminal amino acid sequence was found to be identical to that of Pseudomonas aeruginosa **aliphatic amidase**.

Tags: Comparative Study

Descriptors: *Amidohydrolases--genetics--GE; *Bacterial Proteins
--genetics--GE; *Brevibacterium--enzymology--EN; Amidohydrolases--isolation
and purification--IP; Amino Acid Sequence; Bacterial Proteins--isolation
and purification--IP; Brevibacterium--genetics--GE; Chromatography, High
Pressure Liquid; Molecular Sequence Data; Pseudomonas aeruginosa--genetics
--GE; Sequence Homology, Nucleic Acid; Species Specificity

CAS Registry No.: 0 (Bacterial Proteins)

Enzyme No.: EC 3.5. (Amidohydrolases); EC 3.5.1.4 (amidase)

Record Date Created: 19920611

Record Date Completed: 19920611

3/9/11

DIALOG(R) File 155:MEDLINE(R)

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08977358 PMID: 1907262

Cloning and DNA sequence of amiC, a new gene regulating expression of the Pseudomonas aeruginosa aliphatic amidase, and purification of the amiC product.

Wilson S; Drew R

Department of Biochemistry, University College London, United Kingdom.

Journal of bacteriology (UNITED STATES) Aug 1991, 173 (16) p4914-21,

ISSN 0021-9193 Journal Code: 2985120R

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

Using in vitro-constructed deletions and subcloned DNA fragments, we have identified a new gene, *amiC*, which regulates expression of the inducible Pseudomonas aeruginosa **aliphatic amidase** activity. The DNA sequence of the gene has been determined, and an open reading frame encoding a polypeptide of 385 amino acids (molecular mass, 42,834 Da) has been identified. A search of sequence libraries has failed to find homologies with other published sequences. The *amiC* translation termination codon (A)TGA overlaps the initiation codon for the downstream *amiR* transcription antitermination factor gene, implying that the *amiCR* operon is coordinately regulated. Disruption of the *amiC* open reading frame by insertion and deletion leads to constitutive amidase synthesis, suggesting that *AmiC* is a negative regulator. This is confirmed by the finding that a broad-host-range expression vector carrying *amiC* (pSW41) represses amidase expression in a series of previously characterized P. aeruginosa

amidase-constitutive mutants. The AmiC polypeptide has been purified from PAC452(pSW41), and N-terminal amino acid sequencing has confirmed the gene identification.

Tags: Support, Non-U.S. Gov't; Support, U.S. Gov't, P.H.S.

Descriptors: *Amidohydrolases--genetics--GE; *Bacterial Proteins
--isolation and purification--IP; *Genes, Regulator--genetics--GE;
*Periplasmic Binding Proteins; *Pseudomonas aeruginosa--genetics--GE;
*Repressor Proteins--isolation and purification--IP; Amidohydrolases
--biosynthesis--BI; Amino Acid Sequence; Bacterial Proteins--genetics--GE;
Base Sequence; Enzyme Induction; Escherichia coli--metabolism--ME; Gene
Expression Regulation, Bacterial; Molecular Sequence Data; Mutation
--genetics--GE; Plasmids--genetics--GE; Pseudomonas aeruginosa--enzymology
--EN; Repressor Proteins--genetics--GE; Restriction Mapping
Molecular Sequence Databank No.: GENBANK/M43175; GENBANK/M74478;
GENBANK/M74479; GENBANK/M74480; GENBANK/M74481; GENBANK/M74482;
GENBANK/M74483; GENBANK/M74484; GENBANK/S45931; GENBANK/S45975;
GENBANK/X13776

CAS Registry No.: 0 (Bacterial Proteins); 0 (Periplasmic Binding
Proteins); 0 (Plasmids); 0 (Repressor Proteins); 142462-53-1 (AmiC
protein, Pseudomonas aeruginosa)

Enzyme No.: EC 3.5. (Amidohydrolases); EC 3.5.1.4 (amidase)

Record Date Created: 19910905

Record Date Completed: 19910905

3/9/12

DIALOG(R) File 155:MEDLINE(R)

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08374586 PMID: 2513374

**Positive control of Pseudomonas aeruginosa amidase synthesis is mediated
by a transcription anti-termination mechanism.**

Drew R; Lowe N

Department of Biochemistry, University College London, UK.

Journal of general microbiology (ENGLAND) Apr 1989, 135 (Pt 4)
p817-23, ISSN 0022-1287 Journal Code: 0375371

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

The DNA sequence of the region upstream from the amidase structural gene (amiE) of Pseudomonas aeruginosa indicates that amidase (EC 3.5.1.4) is transcribed from an Escherichia coli-like promoter located 150 bp before the amiE translation initiation codon. The sequence between the promoter and the coding sequence includes a single open reading frame followed by an E. coli-like rho-independent transcription terminator. A deletion within the presumed terminator region which disrupts the potential stem/loop formation leads to high constitutive amidase expression which is independent of the product of the regulator gene (amiR). It is proposed that the catabolic **aliphatic amidase** of P. aeruginosa is regulated by a transcription anti-termination mechanism. The magnoconstitutive mutant PAC433 has promoter and terminator sequences identical to the wild-type PAC1 but contains a single base pair change in the amiE gene ribosome-binding site.

Tags: Support, Non-U.S. Gov't

Descriptors: *Amidohydrolases--biosynthesis--BI; *Pseudomonas aeruginosa
--genetics--GE; *Transcription, Genetic; Amidohydrolases--genetics--GE;
Base Sequence; DNA, Bacterial--analysis--AN; Molecular Sequence Data;
Plasmids; Pseudomonas aeruginosa--enzymology--EN; Restriction Mapping

Molecular Sequence Databank No.: GENBANK/M25262

CAS Registry No.: 0 (DNA, Bacterial); 0 (Plasmids)

Enzyme No.: EC 3.5. (Amidohydrolases); EC 3.5.1.4 (amidase)

Record Date Created: 19900126

Record Date Completed: 19900126

3/9/13

DIALOG(R) File 155:MEDLINE(R)

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08102032 PMID: 2495988

Nucleotide sequence of the aliphatic amidase regulator gene (amiR) of Pseudomonas aeruginosa.

Lowe N; Rice P M; Drew R E

Department of Biochemistry, University College London, England.

FEBS letters (NETHERLANDS) Mar 27 1989, 246 (1-2) p39-43, ISSN

0014-5793 Journal Code: 0155157

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

The nucleotide sequence of a 1001 bp ClaI/XhoI DNA fragment encoding the amidase regulator gene (amiR) from Pseudomonas aeruginosa has been determined. The sequence derives from strain PAC433, a constitutive high expressing amidase mutant, and contains two overlapping open reading frames. Analysis of the sequence has identified one of the reading frames as amiR. The gene encodes a 196 amino acid polypeptide which shows a strong bias towards codons with G or C in the third position. The amiR gene shows no sequence homology with other bacterial regulator proteins.

Tags: Support, Non-U.S. Gov't

Descriptors: *Amidohydrolases--genetics--GE; *Genes, Bacterial; *Genes, Regulator; *Pseudomonas aeruginosa--genetics--GE; Amino Acid Sequence; Base Sequence; Codon; Deoxyribonucleases, Type II Site-Specific; Molecular Sequence Data; Molecular Weight; Pseudomonas aeruginosa--enzymology--EN; Translation, Genetic

Molecular Sequence Databank No.: GENBANK/X13776

CAS Registry No.: 0 (Codon)

Enzyme No.: EC 3.1.21.- (endodeoxyribonuclease ClaI); EC 3.1.21.- (endodeoxyribonuclease XhoI); EC 3.1.21.4 (Deoxyribonucleases, Type II Site-Specific); EC 3.5. (Amidohydrolases); EC 3.5.1.4 (amidase)

Record Date Created: 19890608

Record Date Completed: 19890608

3/9/14

DIALOG(R) File 155:MEDLINE(R)

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07448695 PMID: 3108030

The nucleotide sequence of the amiE gene of Pseudomonas aeruginosa.

Brammar W J; Charles I G; Matfield M; Liu C P; Drew R E; Clarke P H

FEBS letters (NETHERLANDS) May 11 1987, 215 (2) p291-4, ISSN

0014-5793 Journal Code: 0155157

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

The nucleotide sequence of the amiE gene, encoding the **aliphatic amidase** of Pseudomonas aeruginosa, has been determined. The sequence of 1038 nucleotides shows a strong bias in favour of codons with G or C in the third position, and only 44 different codons are utilised.

Tags: Support, Non-U.S. Gov't

Descriptors: *Amidohydrolases--genetics--GE; *Genes, Bacterial; *Genes, Structural; *Pseudomonas aeruginosa--genetics--GE; Base Sequence; Codon --analysis--AN; DNA, Bacterial--analysis--AN; RNA, Messenger--analysis--AN; Templates, Genetic

CAS Registry No.: 0 (Codon); 0 (DNA, Bacterial); 0 (RNA, Messenger)

Enzyme No.: EC 3.5. (Amidohydrolases); EC 3.5.1.4 (amidase)

Record Date Created: 19870626

Record Date Completed: 19870626

3/9/15

DIALOG(R) File 155:MEDLINE(R)

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07448694 PMID: 3108029

The amino acid sequence of the aliphatic amidase from *Pseudomonas aeruginosa*.

Ambler R P; Auffret A D; Clarke P H
FEBS letters (NETHERLANDS) May 11 1987, 215 (2) p285-90, ISSN
0014-5793 Journal Code: 0155157
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed
Subfile: INDEX MEDICUS

Amino acid sequence studies show that the **aliphatic amidase** (EC 3.5.1.4) from *Pseudomonas aeruginosa* PAC142 consists of a single polypeptide chain of 346 residues, giving an Mr of 38,400. The evidence from the amino acid studies is in complete agreement with that deduced from the DNA sequence of the *amiE* gene. Studies of the protein from *Pseudomonas putida* A87 show that it differs from the *Ps. aeruginosa* protein by about 30 amino acid substitutions. It now becomes possible to relate changes in the enzyme which result in altered specificity to structural changes in the protein.

Tags: Support, Non-U.S. Gov't
Descriptors: *Amidohydrolases--analysis--AN; **Pseudomonas aeruginosa*--enzymology--EN; Amino Acid Sequence; Peptide Fragments--analysis--AN
CAS Registry No.: 0 (Peptide Fragments)
Enzyme No.: EC 3.5. (Amidohydrolases); EC 3.5.1.4 (amidase)
Record Date Created: 19870626
Record Date Completed: 19870626

3/9/16

DIALOG(R) File 155: MEDLINE(R)

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07316491 PMID: 3098906

A comparative study of acquired amidase activity in *Pseudomonas* species.

Wyndham R C; Slater J H
Journal of general microbiology (ENGLAND) Aug 1986, 132 (Pt 8)
p2195-204, ISSN 0022-1287 Journal Code: 0375371
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed
Subfile: INDEX MEDICUS

Pseudomonas putida PP3 carrying dehalogenases I and II and *Pseudomonas aeruginosa* PAU3 carrying dehalogenase I coded for by plasmid pUU2 were able to grow on 2-monochloropropionic acid (2MCPA). Neither strain utilized 2-chloropropionamide (2CPA) as a carbon or nitrogen source for growth. Mutations in both strains to 2Cpa⁺ phenotypes (designated *P. putida* PPW3 and *P. aeruginosa* PAU5, respectively) involved the expression of an acquired 2CPA-amidase activity. The amidase followed by dehalogenase reactions in these strains constituted a novel metabolic pathway for growth on 2CPA. *P. putida* PPW3 synthesized a constitutive amidase of molecular mass 59 kDa consisting of two identical subunits of 29 kDa. For those amides tested this acquired enzyme was most active against chlorinated aliphatic amides, although substrate affinities (Km) and maximum rates of activity (Vmax) were poor. *P. aeruginosa* PAU5 acquired a 2Cpa⁺ phenotype by overproducing the A-amidase normally used by this species to hydrolyse **aliphatic** amides. The A- amidase had only slight activity towards 2CPA. However, with constitutive synthesis the mutant grew on the chlorinated substrates. Chloroacetamide (CAA) was a toxic substrate analogue for these *Pseudomonas* strains. A strain resistant to CAA was isolated from *P. aeruginosa* PAU5 when exposed to 1-10 mM-CAA. This mutant, *P. aeruginosa* PAU6, synthesized an inducible A-amidase. CAA-resistance depended upon the simultaneous expression of CAA-inducible amidase and dehalogenase activities.

Tags: Comparative Study; Support, Non-U.S. Gov't
Descriptors: *Aminohydrolases--metabolism--ME; **Pseudomonas*--enzymology--EN; Acetamides--metabolism--ME; Acetyltransferases--metabolism--ME;

Aminohydrolases--isolation and purification--IP; Mutation; Phenotype;
Pseudomonas--growth and development--GD; Pseudomonas aeruginosa--enzymology
--EN; Pseudomonas aeruginosa--growth and development--GD
CAS Registry No.: 0 (Acetamides); 79-07-2 (chloroacetamide)
Enzyme No.: EC 2.3.1. (Acetyltransferases); EC 3.5.4.
(Aminohydrolases)
Record Date Created: 19870219
Record Date Completed: 19870219

3/9/17

DIALOG(R) File 155:MEDLINE(R)

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06715270 PMID: 6440948

Complementation analysis of the aliphatic amidase genes of Pseudomonas aeruginosa.

Drew R

Journal of general microbiology (ENGLAND) Dec 1984, 130 (Pt 12)
p3101-11, ISSN 0022-1287 Journal Code: 0375371

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

A plasmid, pCL34, capable of autonomous replication in Escherichia coli and Pseudomonas aeruginosa has been constructed which carries the promoter and structural gene (amiE) for P. aeruginosa amidase, but not the regulator gene (amiR). Plasmid pCL34 has been mobilized from E. coli to P. aeruginosa using the broad host range plasmid RP4. Complementation studies were performed in P. aeruginosa strains carrying various amidase mutations. Measurements of amidase activity in the recipients under inducing, non-inducing and repressing conditions showed trans-complementation by the chromosomally located regulator gene product. These results confirmed the positive control model for amidase gene expression. Levels of amidase expression seen during these studies were approximately threefold higher than in the parental, amidase-positive strains.

Tags: Support, Non-U.S. Gov't

Descriptors: *Amidohydrolases--genetics--GE; *Genes, Bacterial; *Genes, Structural; *Pseudomonas aeruginosa--genetics--GE; Chromosome Mapping; Gene Expression Regulation; Genetic Complementation Test; Phenotype; Plasmids; Pseudomonas aeruginosa--enzymology--EN; Transformation, Bacterial

CAS Registry No.: 0 (Plasmids)

Enzyme No.: EC 3.5. (Amidohydrolases)

Record Date Created: 19850314

Record Date Completed: 19850314

3/9/18

DIALOG(R) File 155:MEDLINE(R)

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05674138 PMID: 6793036

Chloroacetone as an active-site-directed inhibitor of the aliphatic amidase from Pseudomonas aeruginosa.

Hollaway M R; Clarke P H; Ticho T

Biochemical journal (ENGLAND) Dec 1 1980, 191 (3) p811-26, ISSN 0264-6021 Journal Code: 2984726R

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

1. Chloroacetone (I) was shown to be an active-site-directed inhibitor of the **aliphatic amidase** (EC 3.5.1.4) from Pseudomonas aeruginosa strain PAC142.2. This inhibitor reacted with the enzyme in two stages: the first involving the reversible formation of an enzymically inactive species, EI, and the second the formation of a species, EX, from which enzymic activity could not be recovered. 3. Different types of kinetic experiment were

conducted to test conformity of the reaction to the scheme: $E + I \xrightleftharpoons[k_{-1}]{k_{+1}} EI \xrightarrow{k_{+2}} EX$ A computer-based analysis of the results was carried out and values of the individual rate constants were determined. 4. No direct evidence for a binding step before the formation of EI could be obtained, as with $[E]_0$ Less Than $[I]_0$ the observed first-order rate constant for the formation of EI was directly proportional to the concentration of chloroacetone up to 1.2 mM (above this concentration the reaction became too rapid to follow even by the stopped-flow method developed to investigate fast inhibition). 5. The value of k_{+1} exhibited a bell-shaped pH-dependency with a maximum value of about $3 \times 10(3) \text{ M}^{-1} \text{ S}^{-1}$ at pH6 and apparent pKa values of 7.8 and about 4.8.6. The values of k_{-1} and k_{+2} were similar and changed with the time of reaction from values of about $3 \times 10(-3) \text{ S}^{-1}$ (pH8.6) at short times to about one-sixth this value for longer periods of incubation. In this respect the simple reaction scheme is insufficient to describe the inhibition process. 7. The overall inhibition reaction is rapid, whether it is considered in relation to the expected chemical reactivity of chloroacetone, the rate of reaction of other enzymes with substrate analogues containing the chloromethyl group, or the rate of the amidase-catalysed hydrolysis of N-methylacetamide, a substrate that is nearly isosteric with chloroacetone. 8. Acetamide protected the amidase from inhibition by chloroacetone, and the concentration-dependence of the protection gave a value of an apparent dissociation constant similar to the K_m value for this substrate. 9. Addition of acetamide to solutions of the species EI led to a slow recovery of activity. Recovery of active enzyme was also observed after dilution of a solution of EI in the absence of substrate. 10. The species EI is considered not to be a simple adsorption complex, and the possibilities are discussed that it may be a tetrahedral carbonyl adduct, a Schiff base (azomethine) or a complex in which the enzyme has undergone a structural change. The species EX is probably a derivative in which there is a covalent bond between a group in the enzyme and the C-1 atom of the inhibitor.

Descriptors: *Acetone--analogs and derivatives--AA; *Amidohydrolases--antagonists and inhibitors--AI; *Pseudomonas aeruginosa--enzymology--EN; Acetamides--pharmacology--PD; Acetone--pharmacology--PD; Binding Sites; Kinetics; Models, Chemical

CAS Registry No.: 0 (Acetamides); 67-64-1 (Acetone); 78-95-5 (chloroacetone)

Enzyme No.: EC 3.5. (Amidohydrolases); EC 3.5.1.4 (amidase)

Record Date Created: 19811119

Record Date Completed: 19811119

3/9/19

DIALOG(R) File 155:MEDLINE(R)

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05204041 PMID: 118234

Molecular basis of altered enzyme specificities in a family of mutant amidases from Pseudomonas aeruginosa.

Paterson A; Clarke P H

Journal of general microbiology (ENGLAND) Sep 1979, 114 (1) p75-85,

ISSN 0022-1287 Journal Code: 0375371

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

A family of mutant amidases has been derived by experimental evolution of the **aliphatic amidase** of Pseudomonas aeruginosa strain PAC1. Mutation *amiE16*, in the structural gene for the enzyme, results in the production of the mutant B amidase by strain B6. This strain, unlike the wild-type, can utilize butyramide for growth. Strain B6 gave rise by a single mutational event to strain V9, utilizing valeramide, and strain PhB3, utilizing phenylacetamide. Strain V9 was not itself able to utilize phenylacetamide but gave rise by mutation to the phenylacetamide-utilizing mutant PhV1. Peptide 108 was isolated from chymotryptic digests of mutant amidases from strains B6, PhB3 and PhV1, but could not be detected in chymotryptic digests of the wild-type amidase. The sequence of peptide 108 was

established as Met-Arg-His-Gly-Asp-Ile-Phe. Thermolytic digests of mutant amidases from strains B6, PhB3, PhV1 and V9 were compared with digests of the wild-type amidase. A peptide of the composition Met, Arg, His, Gly2, Asp3, Ile, Ser3, Thr, Val was found in the digest of the wild-type amidase and was replaced in the digests of the mutant amidases by a peptide of the composition Met, Arg, His, Gly2, Asp3, Ile, Ser3, Thr, Val, Phe. Mutation amiE16 is common to the four mutant enzymes and can be accounted for by the mutation Ser leads to Phe. The sequence of the chymotryptic peptide corresponds with the N-terminal sequence of the amidase protein, and can also be related to the thermolysin peptides. It is concluded that mutation amiE16 is a Ser leads to Phe change at position 7 from the N-terminus and the effect of this on the enzyme conformation is discussed.

Descriptors: *Amidohydrolases--metabolism--ME; *Pseudomonas aeruginosa --enzymology--EN; Amidohydrolases--genetics--GE; Amino Acid Sequence; Chromatography, Gel; Chymotrypsin; Genes, Structural; Mutation; Peptide Fragments--analysis--AN; Pseudomonas aeruginosa--genetics--GE; Substrate Specificity; Thermolysin

CAS Registry No.: 0 (Peptide Fragments)

Enzyme No.: EC 3.4.21.1 (Chymotrypsin); EC 3.4.24.27 (Thermolysin); EC 3.5. (Amidohydrolases)

Record Date Created: 19800317

Record Date Completed: 19800317

3/9/20

DIALOG(R) File 155:MEDLINE(R)

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05202551 PMID: 533765

Local anesthetics block induction of the Pseudomonas alk regulon.

Benson S A

Journal of bacteriology (UNITED STATES) Dec 1979, 140 (3) p1123-5,

ISSN 0021-9193 Journal Code: 2985120R

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

The local anesthetics procaine and piperocaine blocked induction of the plasmid-determined enzymatic activities involved in the metabolism of n-alkanes in Pseudomonas putida. Procaine reversibly inhibited existing alkane hydroxylase activity. Induction of a soluble **aliphatic amidase** activity was not affected. These results support the hypothesis that induction of the plasmid-determined alkane metabolic system in P. putida involves a membrane component(s).

Tags: Support, U.S. Gov't, P.H.S.

Descriptors: *Anesthetics, Local--pharmacology--PD; *Benzoates --pharmacology--PD; *Mixed Function Oxygenases--biosynthesis--BI; *Piperidines--pharmacology--PD; *Procaine--pharmacology--PD; *Pseudomonas --drug effects--DE; Alkanes--metabolism--ME; Amidohydrolases--biosynthesis --BI; Enzyme Induction--drug effects--DE; Mixed Function Oxygenases --genetics--GE; Plasmids; Pseudomonas--genetics--GE; Pseudomonas --metabolism--ME

CAS Registry No.: 0 (Alkanes); 0 (Anesthetics, Local); 0 (Benzoates) ; 0 (Piperidines); 0 (Plasmids); 59-46-1 (Procaine)

Enzyme No.: EC 1.- (Mixed Function Oxygenases); EC 3.5. (Amidohydrolases)

Record Date Created: 19800327

Record Date Completed: 19800327

3/9/21

DIALOG(R) File 155:MEDLINE(R)

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05155937 PMID: 115712

A competition time-course method for following enzymic reactions applied to the hydrolysis of acetamide catalysed by an aliphatic amidase .

Hollaway M R; Ticho T

FEBS letters (NETHERLANDS) Oct 1 1979, 106 (1) p185-8, ISSN
0014-5793 Journal Code: 0155157
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed
Subfile: INDEX MEDICUS
Descriptors: *Amidohydrolases--metabolism--ME; Acetamides; Binding,
Competitive; Hydrolysis; Kinetics; Mathematics; Pseudomonas aeruginosa
--enzymology--EN; Time Factors
CAS Registry No.: 0 (Acetamides)
Enzyme No.: EC 3.5. (Amidohydrolases)
Record Date Created: 19800124
Record Date Completed: 19800124

3/9/22

DIALOG(R) File 155:MEDLINE(R)

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05067535 PMID: 110589

Inhibition of the aliphatic amidase from Pseudomonas aeruginosa by urea and related compounds.

Gregoriou M; Brown P R

European journal of biochemistry / FEBS (GERMANY, WEST) May 2 1979, 96

(1) p101-8, ISSN 0014-2956 Journal Code: 0107600

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

The time-dependent inhibition of amidase from Pseudomonas aeruginosa strain AI 3 by urea, hydroxyurea and cyanate displayed saturation kinetics fitting a model for the reaction sequence in which formation of a complex in a reversible step was followed by an irreversible step. Altered amidases from mutant strains AIU 1N and OUCH 4, selected for their resistance to inhibition of growth by urea and hydroxyurea respectively, had altered kinetic constants for inhibition indicating reduced binding capacity for the inhibitors. The substrate acetamide protected AI 3 amidase against inhibition by urea, and altered K_i values for inhibition of the mutant amidases were paralleled by alterations in K_m values for acetamide indicating that urea acted at the active site. Inhibition of AI 3 amidase involved the binding of one molecule of urea per molecule of enzyme. Urea inhibited amidase slowly regained activity at pH 7.2 through release of urea.

Descriptors: *Amidohydrolases--antagonists and inhibitors--AI;
*Pseudomonas aeruginosa--enzymology--EN; *Urea--pharmacology--PD; Cyanates
--pharmacology--PD; Enzyme Activation; Hydroxyurea--pharmacology--PD;
Kinetics; Molecular Weight

CAS Registry No.: 0 (Cyanates); 127-07-1 (Hydroxyurea); 57-13-6 (Urea)

Enzyme No.: EC 3.5. (Amidohydrolases)

Record Date Created: 19790925

Record Date Completed: 19790925

3/9/23

DIALOG(R) File 155:MEDLINE(R)

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05063754 PMID: 110350

Kinetic mechanism of the aliphatic amidase from Pseudomonas aeruginosa.

Woods M J; Findlater J D; Orsi B A

Biochimica et biophysica acta (NETHERLANDS) Mar 16 1979, 567 (1)
p225-37, ISSN 0006-3002 Journal Code: 0217513

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

The kinetic constants for hydrolysis and transfer (with hydroxylamine as the alternate acceptor) of the **aliphatic amidase** (acylamide amidohydrolase, EC 3.5.1.4) from *Pseudomonas aeruginosa* were determined for a variety of acetyl and propionyl derivatives. The results obtained were consistent with a ping-pong or substitution mechanism. Product inhibition, which was pH dependent, implicated an acyl-enzyme compound as a compulsory intermediate and indicated that ammonia combined additionally with the free enzyme in a dead-end manner. The uncompetitive activation of acetamide hydrolysis by hydroxylamine and the observation that the partitioning of products between acetic acid and acetohydroxamate was linearly dependent on the hydroxylamine concentration substantiated these conclusions and indicated that deacylation was at least partially rate limiting. With propionamide as the acyl donor apparently anomalous results, which included inequalities in certain kinetic constants and a hyperbolic dependence of the partition ratio on the hydroxylamine concentration, could be explained by postulating a compulsory isomerisation of the acyl-enzyme intermediate prior to the transfer reaction.

Descriptors: *Amidohydrolases--metabolism--ME; *Pseudomonas aeruginosa --enzymology--EN; Acetamides; Acetic Acids--pharmacology--PD; Acylation; Amides; Amidohydrolases--antagonists and inhibitors--AI; Binding Sites; Hydrolysis; Hydroxylamines--pharmacology--PD; Kinetics; Models, Chemical; Propionates

CAS Registry No.: 0 (Acetamides); 0 (Acetic Acids); 0 (Amides); 0 (Hydroxylamines); 0 (Propionates)

Enzyme No.: EC 3.5. (Amidohydrolases)

Record Date Created: 19790925

Record Date Completed: 19790925

3/9/24

DIALOG(R) File 155:MEDLINE(R)

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04476995 PMID: 14704

Relationship between culture density and catabolite repression of an inducible aliphatic amidase in a thermophilic bacillus.

Thalenfeld B; Epstein I; Grossowicz N

Biochimica et biophysica acta (NETHERLANDS) Mar 29 1977, 497 (1) p112-21, ISSN 0006-3002 Journal Code: 0217513

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

A direct correlation between the absorbance of a thermophilic bacillus and specific amidase activity was observed, which was found to depend on the cell density of the culture rather than on the time of contact of the culture with the inducer. Dilution of high density cultures caused the specific amidase activity to decrease. Environmental factors such as pH, concentration of inducer or degree of aeration, and level of NH₄ and glutamate had no effect on amidase synthesis. The decrease in amidase activity upon dilution could not be ascribed to destruction by oxygen or by inactivation or decay. Several lines of evidence suggest that catabolite repression is responsible for the phenomenon described. Succinate-grown cultures gave a stronger dilution effect than glutamate-grown cells. The mutant strain E-21, relatively resistant to catabolite repression, did not show the characteristic dilution effect nor the direct correlation between absorbance and specific amidase activity.

Descriptors: *Acetamides--pharmacology--PD; *Amidohydrolases--metabolism--ME; *Bacteria--enzymology--EN; Amidohydrolases--biosynthesis--BI; Ammonium Compounds--pharmacology--PD; Bacteria--growth and development--GD; Culture Media; Densitometry; Enzyme Induction; Enzyme Repression; Glutamates--pharmacology--PD; Hydrogen-Ion Concentration; Mutation; Osmolar Concentration

CAS Registry No.: 0 (Acetamides); 0 (Ammonium Compounds); 0 (Culture Media); 0 (Glutamates)

Enzyme No.: EC 3.5. (Amidohydrolases)

Record Date Created: 19770527
Record Date Completed: 19770527

3/9/25

DIALOG(R) File 155:MEDLINE(R)

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04287097 PMID: 932686

Regulatory properties of an inducible aliphatic amidase in a thermophilic bacillus.

Thalenfeld B; Grossowicz N

Journal of general microbiology (ENGLAND) May 1976, 94 (1) p131-41,
ISSN 0022-1287 Journal Code: 0375371

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

A thermophilic bacillus growing on acetamide as both carbon and nitrogen sources produces an inducible amidase. This amidase hydrolysed the following amides in decreasing order of activity, in comparison with acetamide (1.00): propionamide (0.97), fluoroacetamide (0.84), formamide (0.35) and glycine (0.12). Cyanoacetamide, dimethylacetamide, dimethylformamide and urea also induced the synthesis of the amidase, but were not substrates of the enzyme. Studies with protoplasts suggest that the amidase is located in the cytoplasm. Glucose strongly inhibited amidase synthesis; and limiting nitrogen did not release this inhibition. Urea strongly inhibited amidase activity in a competitive manner; but the inhibition caused by iodoacetamide and cyanoacetamide was non-competitive. Both thioacetamide and thiourea were effective inhibitors of enzyme induction. Bacteria grown on a succinate-minimal medium exhibited a lag in amidase synthesis, which could be eliminated by decreasing the concentration of succinate. Acetate- or pyruvate-grown cultures behaved similarly, while those grown on alanine or glutamate exhibited no lag in enzyme induction. In the mutant strain E21, repression of amidase synthesis by glucose was much less evident and no lag for induction was apparent with any of the other carbon sources mentioned.

Descriptors: *Amidohydrolases--biosynthesis--BI; *Bacillus--enzymology--EN; Acetamides--metabolism--ME; Amides--metabolism--ME; Amidohydrolases--metabolism--ME; Bacillus--growth and development--GD; Bacillus--metabolism--ME; Cell-Free System; Cytoplasm--enzymology--EN; Enzyme Induction--drug effects--DE; Enzyme Repression; Glucose--pharmacology--PD; Heat; Kinetics; Protoplasts--enzymology--EN; Thioacetamide--pharmacology--PD; Thiourea--pharmacology--PD; Urea--pharmacology--PD

CAS Registry No.: 0 (Acetamides); 0 (Amides); 50-99-7 (Glucose); 57-13-6 (Urea); 62-55-5 (Thioacetamide); 62-56-6 (Thiourea)

Enzyme No.: EC 3.5. (Amidohydrolases)

Record Date Created: 19760823

Record Date Completed: 19760823

3/9/26

DIALOG(R) File 155:MEDLINE(R)

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04106765 PMID: 170365

Catabolite repression of Pseudomonas aeruginosa amidase: the effect of carbon source on amidase synthesis.

Smyth P F; Clarke P H

Journal of general microbiology (ENGLAND) Sep 1975, 90 (1) p81-90,
ISSN 0022-1287 Journal Code: 0375371

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

Synthesis of the Pseudomonas aeruginosa aliphatic amidase was repressed severely by succinate and malate and less severely by glucose,

acetate or lactate. Amidase synthesis in inducible and constitutive strains was stimulated by cyclic AMP, which also gave partial relief to catabolite repression produced by the addition of lactate to cultures growing in pyruvate medium. Mutants which were resistant to catabolite repression were isolated from succinate+lactamide medium.

Descriptors: *Amidohydrolases--biosynthesis--BI; *Pseudomonas aeruginosa--enzymology--EN; Acetamides--pharmacology--PD; Acetates--pharmacology--PD; Citrates--pharmacology--PD; Cyclic AMP--pharmacology--PD; Enzyme Repression; Glucose--pharmacology--PD; Glycerol--pharmacology--PD; Lactates--pharmacology--PD; Malates--pharmacology--PD; Mutation; Pseudomonas aeruginosa--metabolism--ME; Pyruvates--metabolism--ME; Succinates--pharmacology--PD

CAS Registry No.: 0 (Acetamides); 0 (Acetates); 0 (Citrates); 0 (Lactates); 0 (Malates); 0 (Pyruvates); 0 (Succinates); 50-99-7 (Glucose); 56-81-5 (Glycerol); 60-92-4 (Cyclic AMP)

Enzyme No.: EC 3.5. (Amidohydrolases)

Record Date Created: 19751220

Record Date Completed: 19751220

3/9/27

DIALOG(R) File 155:MEDLINE(R)

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03660624 PMID: 4201665

Transition-state analogs of an aliphatic amidase .

Findlater J D; Orsi B A

FEBS letters (NETHERLANDS) Sep 1 1973, 35 (1) p109-11, ISSN

0014-5793 Journal Code: 0155157

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

Descriptors: *Pseudomonas aeruginosa--enzymology--EN; Acetates; Aldehydes; Amidohydrolases--antagonists and inhibitors--AI; Ammonia; Catalysis; Ethanol; Ethylamines; Hydroxamic Acids; Kinetics

CAS Registry No.: 0 (Acetates); 0 (Aldehydes); 0 (Ethylamines); 0 (Hydroxamic Acids); 64-17-5 (Ethanol); 7664-41-7 (Ammonia)

Enzyme No.: EC 3.5. (Amidohydrolases)

Record Date Created: 19740115

Record Date Completed: 19740115

3/9/28

DIALOG(R) File 155:MEDLINE(R)

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03551524 PMID: 4633800

The subunit structure of the aliphatic amidase from Pseudomonas aeruginosa.

Brown P R; Smyth M J; Clarke P H; Rosemeyer M A

European journal of biochemistry / FEBS (GERMANY, WEST) Apr 2 1973, 34

(1) p177-87, ISSN 0014-2956 Journal Code: 0107600

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

Descriptors: *Amidohydrolases--analysis--AN; *Pseudomonas aeruginosa--enzymology--EN; Acetamides; Alanine--analysis--AN; Amino Acids--analysis--AN; Chloromercuribenzoates; Chromatography, Gel; Cyanogen Bromide; Dicarboxylic Acids; Electrophoresis, Disc; Electrophoresis, Polyacrylamide Gel; Hydrogen-Ion Concentration; Imides; Indicators and Reagents; Macromolecular Systems; Methionine--analysis--AN; Molecular Weight; Osmolar Concentration; Peptides--analysis--AN; Protein Denaturation; Sodium Dodecyl Sulfate; Ultracentrifugation

CAS Registry No.: 0 (Acetamides); 0 (Amino Acids); 0 (Chloromercuribenzoates); 0 (Dicarboxylic Acids); 0 (Imides); 0

(Indicators and Reagents); 0 (Macromolecular Systems); 0 (Peptides);
151-21-3 (Sodium Dodecyl Sulfate); 506-68-3 (Cyanogen Bromide); 56-41-7
(Alanine); 63-68-3 (Methionine)
Enzyme No.: EC 3.5. (Amidohydrolases)
Record Date Created: 19730629
Record Date Completed: 19730629

3/9/29

DIALOG(R) File 155:MEDLINE(R)

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03398192 PMID: 4625925

**Biochemical and immunological comparison of aliphatic amidases
produced by Pseudomonas species.**

Clarke P H

Journal of general microbiology (ENGLAND) Jul 1972, 71 (2) p241-57,

ISSN 0022-1287 Journal Code: 0375371

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

Descriptors: *Amidohydrolases--biosynthesis--BI; *Pseudomonas--enzymology
--EN; Acetamides--metabolism--ME; Antigens; Cell-Free System; Cross
Reactions; Culture Media; Electrophoresis, Starch Gel; Enzyme Induction;
Formamides--metabolism--ME; Genes, Regulator; Genes, Structural; Hydrolases
--analysis--AN; Hydrolysis; Immune Sera; Immunodiffusion; Mutation;
Phenotype; Pseudomonas--metabolism--ME; Pseudomonas aeruginosa--enzymology
--EN; Pseudomonas aeruginosa--immunology--IM; Transferases--analysis--AN

CAS Registry No.: 0 (Acetamides); 0 (Antigens); 0 (Culture Media);
0 (Formamides); 0 (Immune Sera)

Enzyme No.: EC 2. (Transferases); EC 3. (Hydrolases); EC 3.5.
(Amidohydrolases)

Record Date Created: 19720922

Record Date Completed: 19720922

3/9/30

DIALOG(R) File 155:MEDLINE(R)

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02753312 PMID: 5821403

The isolation of an aliphatic amidase from Pseudomonas aeruginosa.

Lilly M D; Clarke P H; Houldsworth M; Currier J A; Dunnill P

Biotechnology and bioengineering (UNITED STATES) May 1969, 11 (3)
p283-92, ISSN 0006-3592 Journal Code: 7502021

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

Descriptors: *Aminohydrolases--isolation and purification--IP;
*Pseudomonas--enzymology--EN; Chromatography, Ion Exchange; Methods;
Precipitation; Technology

Enzyme No.: EC 3.5.4. (Aminohydrolases)

Record Date Created: 19691105

Record Date Completed: 19691105

?b 411

13apr04 12:09:32 User228206 Session D2146.4

\$3.12 0.975 DialUnits File155

\$6.30 30 Type(s) in Format 9

\$6.30 30 Types

\$9.42 Estimated cost File155

\$0.24 TELNET

\$9.66 Estimated cost this search

\$10.69 Estimated total session cost 1.137 DialUnits

File 411:DIALINDEX(R)

DIALINDEX(R)

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*** format unless you enter the SET DETAIL ON command. ***

?sf allscience

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?s aliphatic?/ti and amidase?/ti

Your SELECT statement is:

s aliphatic?/ti and amidase?/ti

Items	File
28	5: Biosis Previews(R)_1969-2004/Apr W1
10	34: SciSearch(R) Cited Ref Sci_1990-2004/Apr W1
1	50: CAB Abstracts_1972-2004/Mar
1	51: Food Sci.&Tech.Abs_1969-2004/Apr W2
1	65: Inside Conferences_1993-2004/Apr W1
6	71: ELSEVIER BIOBASE_1994-2004/Apr W1
16	73: EMBASE_1974-2004/Apr W1
2	98: General Sci Abs/Full-Text_1984-2004/Apr
Examined 50 files	
2	143: Biol. & Agric. Index_1983-2004/Mar
13	144: Pascal_1973-2004/Apr W1
20	155: MEDLINE(R)_1966-2004/Apr W1
2	156: ToxFile_1965-2004/Apr W2
1	162: Global Health_1983-2004/Mar
1	203: AGRIS_1974-2004/Feb
Examined 100 files	
1	292: GEOBASE(TM)_1980-2004/Apr B1
3	340: CLAIMS(R)/US Patent_1950-04/Apr 08
1	342: Derwent Patents Citation Indx_1978-04/200420
1	345: Inpadoc/Fam.& Legal Stat_1968-2003/UD=200414
Examined 150 files	
1	348: EUROPEAN PATENTS_1978-2004/Apr W01
1	349: PCT FULLTEXT_1979-2002/UB=20040408,UT=20040401
4	357: Derwent Biotech Res._1982-2004/Apr W2
>>>Term "TI" is not defined in file 390 and is ignored	
11	390: Beilstein Online_
>>>Term "TI" is not defined in file 398 and is ignored	
12	398: Chemsearch_1957-2004/Mar
25	399: CA SEARCH(R)_1967-2004/UD=14016
12	434: SciSearch(R) Cited Ref Sci_1974-1989/Dec
21	440: Current Contents Search(R)_1990-2004/Apr 13
Examined 200 files	
3	654: US Pat.Full._1976-2004/Apr 06
Examined 250 files	

27 files have one or more items; file list includes 283 files.

One or more terms were invalid in 94 files.

?save temp

Temp SearchSave "TD803" stored

?rf

Your last SELECT statement was:

S ALIPHATIC?/TI AND AMIDASE?/TI

Ref	Items	File
N1	28	5: Biosis Previews(R)_1969-2004/Apr W1
N2	25	399: CA SEARCH(R)_1967-2004/UD=14016
N3	21	440: Current Contents Search(R)_1990-2004/Apr 13
N4	20	155: MEDLINE(R)_1966-2004/Apr W1
N5	16	73: EMBASE_1974-2004/Apr W1
N6	13	144: Pascal_1973-2004/Apr W1
N7	12*	398: Chemsearch_1957-2004/Mar

N8 12 434: SciSearch(R) Cited Ref Sci_1974-1989/Dec
 N9 11* 390: Beilstein Online_
 N10 10 34: SciSearch(R) Cited Ref Sci_1990-2004/Apr W1
 27 files have one or more items; file list includes 283 files.
 * One or more search terms are invalid in this file

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?p

Your last SELECT statement was:

S ALIPHATIC?/TI AND AMIDASE?/TI

Ref	Items	File
N11	6	71: ELSEVIER BIOBASE_1994-2004/Apr W1
N12	4	357: Derwent Biotech Res._1982-2004/Apr W2
N13	3	340: CLAIMS(R)/US Patent_1950-04/Apr 08
N14	3	654: US Pat.Full._1976-2004/Apr 06
N15	2	98: General Sci Abs/Full-Text_1984-2004/Apr
N16	2	143: Biol. & Agric. Index_1983-2004/Mar
N17	2	156: ToxFile_1965-2004/Apr W2
N18	1	50: CAB Abstracts_1972-2004/Mar
N19	1	51: Food Sci.&Tech.Abs_1969-2004/Apr W2
N20	1	65: Inside Conferences_1993-2004/Apr W1

27 files have one or more items; file list includes 283 files.

- Enter P or PAGE for more -

?p

Your last SELECT statement was:

S ALIPHATIC?/TI AND AMIDASE?/TI

Ref	Items	File
N21	1	162: Global Health_1983-2004/Mar
N22	1	203: AGRIS_1974-2004/Feb
N23	1	292: GEOBASE(TM)_1980-2004/Apr B1
N24	1	342: Derwent Patents Citation Indx_1978-04/200420
N25	1	345: Inpadoc/Fam.& Legal Stat_1968-2003/UD=200414
N26	1	348: EUROPEAN PATENTS_1978-2004/Apr W01
N27	1	349: PCT FULLTEXT_1979-2002/UB=20040408,UT=20040401
N28	0	2: INSPEC_1969-2004/Apr W1
N29	0	6: NTIS_1964-2004/Apr W1
N30	0	8: Ei Compendex(R)_1970-2004/Apr W1

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 \$3.97 Estimated cost File411
 \$0.75 TELNET
 \$4.72 Estimated cost this search
 \$15.41 Estimated total session cost 2.900 DialUnits

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File 155:MEDLINE(R) 1966-2004/Apr W1

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File 5:Biosis Previews(R) 1969-2004/Apr W1

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File 399:CA SEARCH(R) 1967-2004/UD=14016

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File 440:Current Contents Search(R) 1990-2004/Apr 13

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File 144:Pascal 1973-2004/Apr W1

(c) 2004 INIST/CNRS

File 357:Derwent Biotech Res. _1982-2004/Apr W2
 (c) 2004 Thomson Derwent & ISI
 File 340:CLAIMS(R)/US Patent 1950-04/Apr 08
 (c) 2004 IFI/CLAIMS(R)
***File 340: Annual reload and classification updates delayed due**
to processing issues.
 File 654:US Pat.Full. 1976-2004/Apr 06
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for details. Reassignments current through December 2, 2003.
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 (c) 2004 The HW Wilson Co
 File 156:ToxFile 1965-2004/Apr W2
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 File 50:CAB Abstracts 1972-2004/Mar
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 File 342:Derwent Patents Citation Indx 1978-04/200420
 (c) 2004 Thomson Derwent
 File 348:EUROPEAN PATENTS 1978-2004/Apr W01
 (c) 2004 European Patent Office
 File 349:PCT FULLTEXT 1979-2002/UB=20040408,UT=20040401
 (c) 2004 WIPO/Univentio

Set	Items	Description
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63335 ALIPHATIC?/TI

5968 AMIDASE?/TI

S1 127 ALIPHATIC?/TI AND AMIDASE?/TI

?rd

>>>Duplicate detection is not supported for File 340.

>>>Duplicate detection is not supported for File 654.

>>>Duplicate detection is not supported for File 342.

>>>Duplicate detection is not supported for File 348.

>>>Duplicate detection is not supported for File 349.

>>>Records from unsupported files will be retained in the RD set.

...examined 50 records (50)

>>>Record 440:17307720 ignored; incomplete bibliographic data, not retained in RD set

>>>Record 440:17032337 ignored; incomplete bibliographic data, not retained in RD set

>>>Record 440:13036975 ignored; incomplete bibliographic data, not retained in RD set

>>>Record 440:12725086 ignored; incomplete bibliographic data, not retained in RD set

>>>Record 440:11493316 ignored; incomplete bibliographic data, not retained in RD set

>>>Record 440:9742553 ignored; incomplete bibliographic data, not retained in RD set

>>>Record 440:9089725 ignored; incomplete bibliographic data, not retained in RD set

>>>Record 440:8865141 ignored; incomplete bibliographic data, not retained in RD set

>>>Record 440:8035998 ignored; incomplete bibliographic data, not retained in RD set

>>>Record 440:6558298 ignored; incomplete bibliographic data, not retained in RD set

>>>Record 440:6249500 ignored; incomplete bibliographic data, not retained in RD set

>>>Record 440:6220878 ignored; incomplete bibliographic data, not retained in RD set

>>>Record 440:3035968 ignored; incomplete bibliographic data, not retained in RD set

>>>Record 440:2233499 ignored; incomplete bibliographic data, not retained in RD set

...examined 50 records (100)

...completed examining records

S2 48 RD (unique items)

?t s2/6/all

2/6/1 (Item 1 from file: 155)

13675690 PMID: 9364923

Identification and characterization of an aliphatic amidase in *Helicobacter pylori*.

Sep 1997

2/6/2 (Item 2 from file: 155)

12684768 PMID: 7607322

Pseudomonas aeruginosa aliphatic amidase is related to the nitrilase/cyanide hydratase enzyme family and Cys166 is predicted to be the active site nucleophile of the catalytic mechanism.

Jul 3 1995

2/6/3 (Item 3 from file: 155)

12503813 PMID: 14500481

Presence of active aliphatic amidases in *Helicobacter* species able to colonize the stomach.

Oct 2003

2/6/4 (Item 4 from file: 155)

11451002 PMID: 11556902

Aliphatic and enantioselective amidases : from hydrolysis to acyl transfer activity.

Sep 2001

2/6/5 (Item 5 from file: 155)

11281780 PMID: 11359566

The AmiE aliphatic amidase and AmiF formamidase of *Helicobacter pylori*: natural evolution of two enzyme paralogues.

May 2001

2/6/6 (Item 6 from file: 155)

10616641 PMID: 10720437

Amino acid homologies between human biotinidase and bacterial aliphatic amidases : putative identification of the active site of biotinidase.

Feb 2000

2/6/7 (Item 7 from file: 155)

08977358 PMID: 1907262

Cloning and DNA sequence of *amiC*, a new gene regulating expression of the *Pseudomonas aeruginosa* aliphatic amidase , and purification of the *amiC* product.

Aug 1991

2/6/8 (Item 8 from file: 155)

08102032 PMID: 2495988

Nucleotide sequence of the aliphatic amidase regulator gene (*amiR*) of *Pseudomonas aeruginosa*.

Mar 27 1989

2/6/9 (Item 9 from file: 155)

07448694 PMID: 3108029

The amino acid sequence of the aliphatic amidase from *Pseudomonas aeruginosa*.

May 11 1987

2/6/10 (Item 10 from file: 155)

06715270 PMID: 6440948

Complementation analysis of the aliphatic amidase genes of *Pseudomonas aeruginosa*.

Dec 1984

2/6/11 (Item 11 from file: 155)

05674138 PMID: 6793036

Chloroacetone as an active-site-directed inhibitor of the aliphatic amidase from *Pseudomonas aeruginosa*.

Dec 1 1980

2/6/12 (Item 12 from file: 155)

05155937 PMID: 115712

A competition time-course method for following enzymic reactions applied to the hydrolysis of acetamide catalysed by an aliphatic amidase.

Oct 1 1979

2/6/13 (Item 13 from file: 155)

05067535 PMID: 110589

Inhibition of the aliphatic amidase from *Pseudomonas aeruginosa* by urea and related compounds.

May 2 1979

2/6/14 (Item 14 from file: 155)

05063754 PMID: 110350

Kinetic mechanism of the aliphatic amidase from *Pseudomonas aeruginosa*.

Mar 16 1979

2/6/15 (Item 15 from file: 155)

04476995 PMID: 14704

Relationship between culture density and catabolite repression of an inducible aliphatic amidase in a thermophilic bacillus.

Mar 29 1977

2/6/16 (Item 16 from file: 155)

04287097 PMID: 932686

Regulatory properties of an inducible aliphatic amidase in a thermophilic bacillus.

May 1976

2/6/17 (Item 17 from file: 155)

03660624 PMID: 4201665

Transition-state analogs of an aliphatic amidase.

Sep 1 1973

2/6/18 (Item 18 from file: 155)

03551524 PMID: 4633800

The subunit structure of the aliphatic amidase from *Pseudomonas aeruginosa*.

Apr 2 1973

2/6/19 (Item 19 from file: 155)

03398192 PMID: 4625925

Biochemical and immunological comparison of aliphatic amidases produced by *Pseudomonas* species.

Jul 1972

2/6/20 (Item 20 from file: 155)

02753312 PMID: 5821403

The isolation of an aliphatic amidase from *Pseudomonas aeruginosa*.
May 1969

2/6/21 (Item 1 from file: 5)

0013215382 BIOSIS NO.: 200100387221

Helicobacter aliphatic amidase AmiE polypeptides, and DNA sequences
encoding those polypeptides
2001

2/6/22 (Item 2 from file: 5)

0011231256 BIOSIS NO.: 199800025503

The aliphatic amidase : Another way to produce ammonia in *H. pylori*?
1997

2/6/23 (Item 3 from file: 5)

0003552704 BIOSIS NO.: 198273056631

UTILIZATION OF ALIPHATIC AMIDES AND FORMATION OF 2 DIFFERENT AMIDASES
BY *ALCALIGENES-EUTROPHUS*
1981

2/6/24 (Item 4 from file: 5)

0003243180 BIOSIS NO.: 198171062139

CHLORO ACETONE AS AN ACTIVE SITE DIRECTED INHIBITOR OF THE ALIPHATIC
AMIDASE EC-3.5.1.4 FROM *PSEUDOMONAS-AERUGINOSA*
1980

2/6/25 (Item 5 from file: 5)

0002800018 BIOSIS NO.: 198018039009

A COMPETITION TIME COURSE METHOD FOR FOLLOWING ENZYMIC REACTIONS APPLIED TO
THE HYDROLYSIS OF ACETAMIDE CATALYZED BY AN ALIPHATIC AMIDASE
EC-3.5.1.4
1979

2/6/26 (Item 6 from file: 5)

0002713001 BIOSIS NO.: 197968024500

KINETIC MECHANISM OF THE ALIPHATIC AMIDASE EC-3.5.1.4 FROM
PSEUDOMONAS-AERUGINOSA
1979

2/6/27 (Item 7 from file: 5)

0002512657 BIOSIS NO.: 197916021652

PROPERTIES OF AN INDUCIBLE ALIPHATIC AMIDASE FROM A THERMOPHILIC
BACILLUS
1978

2/6/28 (Item 8 from file: 5)

0001773358 BIOSIS NO.: 197612039497

SELECTIVE INHIBITION AND THE KINETIC MECHANISM OF THE ALIPHATIC AMIDASE
EC-3.5.1.4 OF *PSEUDOMONAS-AERUGINOSA*
1974

2/6/29 (Item 9 from file: 5)

0001240272 BIOSIS NO.: 197356056714

THE SUBUNIT STRUCTURE OF THE ALIPHATIC AMIDASE EC-3.5.1.4 FROM
PSEUDOMONAS-AERUGINOSA

1973

2/6/30 (Item 10 from file: 5)
0001123871 BIOSIS NO.: 197355010341
BIOCHEMICAL AND IMMUNOLOGICAL COMPARISON OF ALIPHATIC AMIDASES PRODUCED
BY PSEUDOMONAS-SPP
1972

2/6/31 (Item 11 from file: 5)
0000445043 BIOSIS NO.: 197051041589
FORM AMIDASE IN GUINEA-PIG LIVER PART 2 EFFECT OF ALIPHATIC ALCOHOLS
1969

2/6/32 (Item 12 from file: 5)
0000398848 BIOSIS NO.: 197006085394
THE ALIPHATIC AMIDASES OF PSEUDOMONAS-AERUGINOSA
BOOK TITLE: ROSE, A. H. AND J. F. WILKINSON (EDITED BY). ADVANCES IN
MICROBIAL PHYSIOLOGY, VOL. 4. XI + 353P. ILLUS. ACADEMIC PRESS INC.,
LTD.: LONDON, ENGLAND; NEW YORK, N.Y., U.S.A
1970

2/6/33 (Item 1 from file: 399)
DIALOG(R) File 399:(c) 2004 American Chemical Society. All rts. reserv.

Selective inhibition and the kinetic mechanism of the aliphatic amidase
of Pseudomonase aeruginosa

2/6/34 (Item 1 from file: 144)
03352281 PASCAL No.: 81-0392478
CHLOROACETONE AS AN ACTIVE -RITE-DIRECTED INHIBITOR OF THE ALIPHATIC
AMIDASE FROM PSEUDOMONAS AERUGINOSA
1980

2/6/35 (Item 1 from file: 357)
0312191 DBR Accession No.: 2003-13331
Purification, cloning, sequencing and over-expression in Escherichia coli
of a regioselective aliphatic nitrilase from Acidovorax facilis 72W -
Acidovorax facilis stereospecific nitrile-hydratase and nitrile-
amidase isolation involving vector plasmid pET-mediated nitrilase gene
transfer and expression in Escherichia coli 2003

2/6/36 (Item 2 from file: 357)
0230013 DBR Accession No.: 99-00114
New Helicobacter sp. aliphatic amidase AmiE polypeptides and their
encoding sequence - Helicobacter pylori recombinant protein
preparation, vector expression in host cell and DNA probe and
monoclonal antibody, used for infection diagnosis, recombinant vaccine
or therapy 1998

2/6/37 (Item 3 from file: 357)
0203740 DBR Accession No.: 96-14511
Utilization of acetonitrile and other aliphatic nitriles by a Candida
famata strain - acetonitrile degradation using nitrile-hydratase and
amidase activity 1996

2/6/38 (Item 4 from file: 357)
0001358 DBR Accession No.: 82-00358
Aliphatic nitrile hydratase from Arthrobacter sp.J-1 purification and
characterization - and amidase production; catalysis of acetonitrile
hydrolysis to form acetamide 1982

2/6/39 (Item 1 from file: 340)

3528971

C/HELICOBACTER ALIPHATIC AMIDASE AMIE POLYPEPTIDES, AND DNA SEQUENCES
ENCODING THOSE POLYPEPTIDES; SCREENING BY CONTACTING ENZYME WITH
COMPOUND, AND SELECTING COMPOUND WHICH INHIBITS ENZYME ACTIVITY;
ANTIULCER AGENTS; BACTERICIDES

2/6/40 (Item 2 from file: 340)

3168988

C/PREPARATION OF LACTAMS FROM ALIPHATIC ALPHA, OMEGA-DINITILES; ISOLATED
COMAMONAS TESTOSTERONI 5-MGAM-4D WITH NITRILE HYDRATASE AND AMIDASE
ACTIVITIES; FOR HIGH YIELD WITH HIGH REGIOSELECTIVITY AND BY PRODUCT
INHIBITION

2/6/41 (Item 3 from file: 340)

3096789

C/PREPARATION OF LACTAMS FROM ALIPHATIC ALPHA, OMEGA-DINITRILES;
CONTACTING DINITRILE IN AQUEOUS MIXTURE WITH ENZYME CATALYST HAVING
ALIPHATIC NITRILASE ACTIVITY OR COMBINATION OF NITRILE HYDRATASE AND
AMIDASE ACTIVITY, CONTACTING PRODUCT WITH HYDROGEN AND HYDROGENATION
CATALYST TO PRODUCE LACTAM

2/6/42 (Item 1 from file: 654)

4525521 **IMAGE Available

Derwent Accession: 1998-557106

Utility

C/ Helicobacter aliphatic amidase Amie polypeptides, and DNA sequences
encoding those polypeptides
; SCREENING BY CONTACTING ENZYME WITH COMPOUND, AND SELECTING COMPOUND
WHICH INHIBITS ENZYME ACTIVITY; ANTIULCER AGENTS; BACTERICIDES

Fulltext Word Count: 5689

Number of Claims: 2

Exemplary or Independent Claim Number(s): 1

Number of Drawing Sheets: 23

Number of Figures: 12

Number of US cited patent references: 15

Number of non-US cited patent references: 15

Number of non-patent cited references: 26

2/6/43 (Item 2 from file: 654)

4166734

Derwent Accession: 1998-041747

Utility

C/ Preparation of lactams from aliphatic [alpha],[omega]-Dinitiles
; ISOLATED COMAMONAS TESTOSTERONI 5-MGAM-4D WITH NITRILE HYDRATASE AND
AMIDASE ACTIVITIES; FOR HIGH YIELD WITH HIGH REGIOSELECTIVITY AND BY
PRODUCT INHIBITION

Fulltext Word Count: 19383

Number of Claims: 1

Exemplary or Independent Claim Number(s): 1

Number of US cited patent references: 4

Number of non-US cited patent references: 8

Number of non-patent cited references: 20

2/6/44 (Item 3 from file: 654)

4095232

Derwent Accession: 1998-041747

Utility

C/ Preparation of lactams from aliphatic [alpha],[omega]-dinitriles
; CONTACTING DINITRILE IN AQUEOUS MIXTURE WITH ENZYME CATALYST HAVING

ALIPHATIC NITRILASE ACTIVITY OR COMBINATION OF NITRILE HYDRATASE AND
AMIDASE ACTIVITY, CONTACTING PRODUCT WITH HYDROGEN AND HYDROGENATION
CATALYST TO PRODUCE LACTAM

Fulltext Word Count: 20552

Number of Claims: 20

Exemplary or Independent Claim Number(s): 1

Number of US cited patent references: 5

Number of non-US cited patent references: 8

Number of non-patent cited references: 20

2/6/45 (Item 1 from file: 65)

03333046 INSIDE CONFERENCE ITEM ID: CN035225547

Identification of an aliphatic amidase in *H. pylori*

CONFERENCE: Campylobacter, helicobacter & related organisms-
International workshop; 9th (199709)

2/6/46 (Item 1 from file: 342)

03324989 WPI Acc No: 98-557106/47

New Helicobacter aliphatic amidase AmiE polypeptides and their encoding
sequences...

2/6/47 (Item 1 from file: 348)

01000868

HELICOBACTER ALIPHATIC AMIDASE POLYPEPTIDES, DNA SEQUENCES ENCODING
THOSE POLYPEPTIDES AND USES THEREOF

HELICOBACTER ALIPHATISCHE AMIDASE POLYPEPTIDEN, DAFUR KODIERENDE DNA
SEQUENZEN UND DEREN VERWENDUNGEN

POLYPEPTIDES DE L' AMIDASE ALIPHATIQUE AmiE D'i(HELICOBACTER) ET SEQUENCES
D'ADN CODANT LESDITS POLYPEPTIDES

LANGUAGE (Publication,Procedural,Application): English; English; English

2/6/48 (Item 1 from file: 349)

00453630

i(HELICOBACTER) ALIPHATIC AMIDASE POLYPEPTIDES, DNA SEQUENCES ENCODING
THOSE POLYPEPTIDES AND USES THEREOF

POLYPEPTIDES DE L' AMIDASE ALIPHATIQUE AmiE D'i(HELICOBACTER) ET SEQUENCES
D'ADN CODANT LESDITS POLYPEPTIDES

Publication Language: English

Fulltext Availability:

Detailed Description

Claims

Fulltext Word Count: 9017

Publication Year: 1998

?logoff hold

13apr04 12:12:25 User228206 Session D2146.6

\$0.44 0.138 DialUnits File155

\$0.00 20 Type(s) in Format 6

\$0.00 20 Types

\$0.44 Estimated cost File155

\$0.87 0.155 DialUnits File5

\$0.00 12 Type(s) in Format 6

\$0.00 12 Types

\$0.87 Estimated cost File5

\$0.96 0.076 DialUnits File399

\$0.55 1 Type(s) in Format 6

\$0.55 1 Types

\$1.51 Estimated cost File399

\$1.67 0.079 DialUnits File440

\$1.67 Estimated cost File440

\$0.16 0.047 DialUnits File144

\$0.00 1 Type(s) in Format 6

\$0.00 1 Types

\$0.16 Estimated cost File144

\$0.53 0.027 DialUnits File357

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        $0.00  4 Types
$0.53  Estimated cost File357
        $0.97    0.061 DialUnits File340
        $0.75  3 Type(s) in Format  6
        $0.75  3 Types
$1.72  Estimated cost File340
        $0.84    0.143 DialUnits File654
        $0.75  3 Type(s) in Format  6
        $0.75  3 Types
$1.59  Estimated cost File654
        $0.04    0.015 DialUnits File143
$0.04  Estimated cost File143
        $0.11    0.020 DialUnits File156
$0.11  Estimated cost File156
        $0.07    0.015 DialUnits File50
$0.07  Estimated cost File50
        $0.05    0.012 DialUnits File65
        $0.00  1 Type(s) in Format  6
        $0.00  1 Types
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        $0.04    0.015 DialUnits File203
$0.04  Estimated cost File203
        $0.24    0.015 DialUnits File342
        $0.00  1 Type(s) in Format  6
        $0.00  1 Types
$0.24  Estimated cost File342
        $0.26    0.057 DialUnits File348
        $0.25  1 Type(s) in Format  6
        $0.25  1 Types
$0.51  Estimated cost File348
        $0.22    0.047 DialUnits File349
        $0.25  1 Type(s) in Format  6
        $0.25  1 Types
$0.47  Estimated cost File349
        OneSearch, 16 files,  0.919 DialUnits FileOS
$0.24  TELNET
$10.26 Estimated cost this search
$25.67 Estimated total session cost  3.819 DialUnits

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Status: Signed Off. (4 minutes)

Status: Path 1 of [Dialog Information Services via Modem]

Status: Initializing TCP/IP using (UseTelnetProto 1 ServiceID pto-dialog)
Trying 31060000009999...Open

DIALOG INFORMATION SERVICES

PLEASE LOGON:

***** HHHHHHHH SSSSSSS?

Status: Signing onto Dialog

ENTER PASSWORD:

***** HHHHHHHH SSSSSSS? *****

Welcome to DIALOG

Status: Connected

Dialog level 04.02.00D

Reconnected in file OS 13apr04 12:19:02

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* ALL NEW CURRENT YEAR RANGES HAVE BEEN * * *

* * * INSTALLED * * *

SYSTEM:OS - DIALOG OneSearch

File 155:MEDLINE(R) 1966-2004/Apr W1
 (c) format only 2004 The Dialog Corp.
 *File 155: Medline has been reloaded. Accession numbers have changed. Please see HELP NEWS 154 for details.
 File 5:Biosis Previews(R) 1969-2004/Apr W1
 (c) 2004 BIOSIS
 File 399:CA SEARCH(R) 1967-2004/UD=14016
 (c) 2004 American Chemical Society
 *File 399: Use is subject to the terms of your user/customer agreement. Alert feature enhanced for multiple files, etc. See HELP ALERT.
 File 440:Current Contents Search(R) 1990-2004/Apr 13
 (c) 2004 Inst for Sci Info
 File 144:Pascal 1973-2004/Apr W1
 (c) 2004 INIST/CNRS
 File 357:Derwent Biotech Res. 1982-2004/Apr W2
 (c) 2004 Thomson Derwent & ISI
 File 340:CLAIMS(R)/US Patent 1950-04/Apr 08
 (c) 2004 IFI/CLAIMS(R)
 *File 340: Annual reload and classification updates delayed due to processing issues.
 File 654:US Pat.Full. 1976-2004/Apr 06
 (c) Format only 2004 The Dialog Corp.
 *File 654: US published applications now online. See HELP NEWS 654 for details. Reassignments current through December 2, 2003.
 File 143:Biol. & Agric. Index 1983-2004/Mar
 (c) 2004 The HW Wilson Co
 File 156:ToxFile 1965-2004/Apr W2
 (c) format only 2004 The Dialog Corporation
 File 50:CAB Abstracts 1972-2004/Mar
 (c) 2004 CAB International
 File 65:Inside Conferences 1993-2004/Apr W1
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 File 342:Derwent Patents Citation Indx 1978-04/200420
 (c) 2004 Thomson Derwent
 File 348:EUROPEAN PATENTS 1978-2004/Apr W01
 (c) 2004 European Patent Office
 File 349:PCT FULLTEXT 1979-2002/UB=20040408,UT=20040401
 (c) 2004 WIPO/Univentio

Set Items Description

Cost is in DialUnits
 ?ds

Set	Items	Description
S1	127	ALIPHATIC?/TI AND AMIDASE?/TI
S2	48	RD (unique items)
?t s2/9/1 2 7 8 9 10 11 13 14 16 19 22 45		

2/9/1 (Item 1 from file: 155)
 DIALOG(R) File 155:MEDLINE(R)
 (c) format only 2004 The Dialog Corp. All rts. reserv.

13675690 PMID: 9364923

Identification and characterization of an aliphatic amidase in Helicobacter pylori.

Skouloubris S; Labigne A; De Reuse H
 Unite de Pathogenie Bacterienne des Muqueuses, Institut Pasteur, Paris, France.

Molecular microbiology (ENGLAND) Sep 1997, 25 (5) p989-98, ISSN 0950-382X Journal Code: 8712028

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

We report, for the first time, the presence in Helicobacter pylori of an

aliphatic amidase that, like urease, contributes to ammonia production. Aliphatic amidases are cytoplasmic acylamide amidohydrolases (EC 3.5.1.4) hydrolysing short-chain aliphatic amides to produce ammonia and the corresponding organic acid. The finding of an aliphatic amidase in *H. pylori* was unexpected as this enzyme has only previously been described in bacteria of environmental (soil or water) origin. The *H. pylori* amidase gene *amiE* (1017 bp) was sequenced, and the deduced amino acid sequence of *AmiE* (37746Da) is very similar (75% identity) to the other two sequenced aliphatic amidases, one from *Pseudomonas aeruginosa* and one from *Rhodococcus* sp. R312. Amidase activity was measured as the release of ammonia by sonicated crude extracts from *H. pylori* strains and from recombinant *Escherichia coli* strains overproducing the *H. pylori* amidase. The substrate specificity was analysed with crude extracts from *H. pylori* cells grown in vitro; the best substrates were propionamide, acrylamide and acetamide. Polymerase chain reaction (PCR) amplification of an internal *amiE* sequence was obtained with each of 45 different *H. pylori* clinical isolates, suggesting that amidase is common to all *H. pylori* strains. A *H. pylori* mutant (N6-836) carrying an interrupted *amiE* gene was constructed by allelic exchange. No amidase activity could be detected in N6-836. In a N6-urease negative mutant, amidase activity was two- to threefold higher than in the parental strain N6. Crude extracts of strain N6 slowly hydrolysed formamide. This activity was affected in neither the amidase negative strain (N6-836) nor a double mutant strain deficient in both amidase and urease activities, suggesting the presence of an independent discrete formamidase in *H. pylori*. The existence of an aliphatic amidase, a correlation between the urease and amidase activities and the possible presence of a formamidase indicates that *H. pylori* has a large range of possibilities for intracellular ammonia production.

Tags: Comparative Study; Support, Non-U.S. Gov't

Descriptors: *Amidohydrolases--analysis--AN; **Helicobacter pylori* --enzymology--EN; Amino Acid Sequence; Cloning, Molecular; DNA, Recombinant; *Escherichia coli*--enzymology--EN; *Escherichia coli*--genetics--GE; Genes, Structural, Bacterial--genetics--GE; *Helicobacter pylori*--chemistry--CH; *Helicobacter pylori*--genetics--GE; Molecular Sequence Data; Mutation --genetics--GE; Recombinant Proteins--genetics--GE; Recombinant Proteins --metabolism--ME; Sequence Homology, Amino Acid; Substrate Specificity
Molecular Sequence Databank No.: GENBANK/Y12252
CAS Registry No.: 0 (DNA, Recombinant); 0 (Recombinant Proteins)
Enzyme No.: EC 3.5. (Amidohydrolases); EC 3.5.1.4 (amidase)
Record Date Created: 19980129
Record Date Completed: 19980129

2/9/2 (Item 2 from file: 155)

DIALOG(R) File 155:MEDLINE(R)

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12684768 PMID: 7607322

***Pseudomonas aeruginosa* aliphatic amidase is related to the nitrilase/cyanide hydratase enzyme family and Cys166 is predicted to be the active site nucleophile of the catalytic mechanism.**

Novo C; Tata R; Clemente A; Brown P R

Instituto Nacional de Engenharia e Tecnologia Industrial/IBQTA, Queluz, Portugal.

FEBS letters (NETHERLANDS) Jul 3 1995, 367 (3) p275-9, ISSN 0014-5793 Journal Code: 0155157

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

A database search indicated homology between some members of the nitrilase/cyanide hydratase family, *Pseudomonas aeruginosa* and *Rhodococcus erythropolis* amidases and several other proteins, some of unknown function. BLOCK and PROFILE searches confirmed these relationships and showed that four regions of the *P. aeruginosa* amidase had significant homology with corresponding regions of nitrilases. A phylogenetic tree placed the *P. aeruginosa* and *R. erythropolis* amidases in a group with nitrilases but separated other amidases into three groups. The active site cysteine in

nitrilases is conserved in the *P. aeruginosa* amidase indicating that Cys166 is the active site nucleophile.

Tags: Comparative Study; Support, Non-U.S. Gov't

Descriptors: *Amidohydrolases--chemistry--CH; *Pseudomonas aeruginosa --enzymology--EN; Amidohydrolases--metabolism--ME; Amino Acid Sequence; Aminohydrolases--chemistry--CH; Binding Sites; Cysteine--chemistry--CH; Hydro-Lyases--chemistry--CH; Molecular Sequence Data; Phylogeny; Sequence Alignment; Sequence Homology, Amino Acid

CAS Registry No.: 52-90-4 (Cysteine)

Enzyme No.: EC 3.5. (Amidohydrolases); EC 3.5.1.4 (amidase); EC 3.5.4. (Aminohydrolases); EC 3.5.5.1 (nitrilase); EC 4.2.1. (Hydro-Lyases); EC 4.2.1.66 (cyanide hydratase)

Record Date Created: 19950817

Record Date Completed: 19950817

2/9/7 (Item 7 from file: 155)

DIALOG(R) File 155:MEDLINE(R)

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08977358 PMID: 1907262

Cloning and DNA sequence of *amiC*, a new gene regulating expression of the *Pseudomonas aeruginosa* aliphatic amidase, and purification of the *amiC* product.

Wilson S; Drew R

Department of Biochemistry, University College London, United Kingdom.

Journal of bacteriology (UNITED STATES) Aug 1991, 173 (16) p4914-21,

ISSN 0021-9193 Journal Code: 2985120R

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

Using in vitro-constructed deletions and subcloned DNA fragments, we have identified a new gene, *amiC*, which regulates expression of the inducible *Pseudomonas aeruginosa* aliphatic amidase activity. The DNA sequence of the gene has been determined, and an open reading frame encoding a polypeptide of 385 amino acids (molecular mass, 42,834 Da) has been identified. A search of sequence libraries has failed to find homologies with other published sequences. The *amiC* translation termination codon (A)TGA overlaps the initiation codon for the downstream *amiR* transcription antitermination factor gene, implying that the *amiC* operon is coordinately regulated. Disruption of the *amiC* open reading frame by insertion and deletion leads to constitutive amidase synthesis, suggesting that *AmiC* is a negative regulator. This is confirmed by the finding that a broad-host-range expression vector carrying *amiC* (pSW41) represses amidase expression in a series of previously characterized *P. aeruginosa* amidase-constitutive mutants. The *AmiC* polypeptide has been purified from PAC452(pSW41), and N-terminal amino acid sequencing has confirmed the gene identification.

Tags: Support, Non-U.S. Gov't; Support, U.S. Gov't, P.H.S.

Descriptors: *Amidohydrolases--genetics--GE; *Bacterial Proteins --isolation and purification--IP; *Genes, Regulator--genetics--GE; *Periplasmic Binding Proteins; *Pseudomonas aeruginosa--genetics--GE; *Repressor Proteins--isolation and purification--IP; Amidohydrolases --biosynthesis--BI; Amino Acid Sequence; Bacterial Proteins--genetics--GE; Base Sequence; Enzyme Induction; Escherichia coli--metabolism--ME; Gene Expression Regulation, Bacterial; Molecular Sequence Data; Mutation --genetics--GE; Plasmids--genetics--GE; Pseudomonas aeruginosa--enzymology --EN; Repressor Proteins--genetics--GE; Restriction Mapping

Molecular Sequence Databank No.: GENBANK/M43175; GENBANK/M74478; GENBANK/M74479; GENBANK/M74480; GENBANK/M74481; GENBANK/M74482; GENBANK/M74483; GENBANK/M74484; GENBANK/S45931; GENBANK/S45975; GENBANK/X13776

CAS Registry No.: 0 (Bacterial Proteins); 0 (Periplasmic Binding Proteins); 0 (Plasmids); 0 (Repressor Proteins); 142462-53-1 (*AmiC* protein, *Pseudomonas aeruginosa*)

Enzyme No.: EC 3.5. (Amidohydrolases); EC 3.5.1.4 (amidase)

Record Date Created: 19910905

Record Date Completed: 19910905

2/9/8 (Item 8 from file: 155)

DIALOG(R) File 155: MEDLINE(R)

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08102032 PMID: 2495988

Nucleotide sequence of the aliphatic amidase regulator gene (amiR) of *Pseudomonas aeruginosa*.

Lowe N; Rice P M; Drew R E

Department of Biochemistry, University College London, England.

FEBS letters (NETHERLANDS) Mar 27 1989, 246 (1-2) p39-43, ISSN

0014-5793 Journal Code: 0155157

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

The nucleotide sequence of a 1001 bp *Cla*I/*Xho*I DNA fragment encoding the amidase regulator gene (*amiR*) from *Pseudomonas aeruginosa* has been determined. The sequence derives from strain PAC433, a constitutive high expressing amidase mutant, and contains two overlapping open reading frames. Analysis of the sequence has identified one of the reading frames as *amiR*. The gene encodes a 196 amino acid polypeptide which shows a strong bias towards codons with G or C in the third position. The *amiR* gene shows no sequence homology with other bacterial regulator proteins.

Tags: Support, Non-U.S. Gov't

Descriptors: *Amidohydrolases--genetics--GE; *Genes, Bacterial; *Genes, Regulator; **Pseudomonas aeruginosa*--genetics--GE; Amino Acid Sequence; Base Sequence; Codon; Deoxyribonucleases, Type II Site-Specific; Molecular Sequence Data; Molecular Weight; *Pseudomonas aeruginosa*--enzymology--EN; Translation, Genetic

Molecular Sequence Databank No.: GENBANK/X13776

CAS Registry No.: 0 (Codon)

Enzyme No.: EC 3.1.21.- (endodeoxyribonuclease *Cla*I); EC 3.1.21.- (endodeoxyribonuclease *Xho*I); EC 3.1.21.4 (Deoxyribonucleases, Type II Site-Specific); EC 3.5. (Amidohydrolases); EC 3.5.1.4 (amidase)

Record Date Created: 19890608

Record Date Completed: 19890608

2/9/9 (Item 9 from file: 155)

DIALOG(R) File 155: MEDLINE(R)

(c) format only 2004 The Dialog Corp. All rts. reserv.

07448694 PMID: 3108029

The amino acid sequence of the aliphatic amidase from *Pseudomonas aeruginosa*.

Ambler R P; Auffret A D; Clarke P H

FEBS letters (NETHERLANDS) May 11 1987, 215 (2) p285-90, ISSN

0014-5793 Journal Code: 0155157

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

Amino acid sequence studies show that the aliphatic amidase (EC 3.5.1.4) from *Pseudomonas aeruginosa* PAC142 consists of a single polypeptide chain of 346 residues, giving an Mr of 38,400. The evidence from the amino acid studies is in complete agreement with that deduced from the DNA sequence of the *amiE* gene. Studies of the protein from *Pseudomonas putida* A87 show that it differs from the *Ps. aeruginosa* protein by about 30 amino acid substitutions. It now becomes possible to relate changes in the enzyme which result in altered specificity to structural changes in the protein.

Tags: Support, Non-U.S. Gov't

Descriptors: *Amidohydrolases--analysis--AN; **Pseudomonas aeruginosa*--enzymology--EN; Amino Acid Sequence; Peptide Fragments--analysis--AN

CAS Registry No.: 0 (Peptide Fragments)

Enzyme No.: EC 3.5. (Amidohydrolases); EC 3.5.1.4 (amidase)

Record Date Created: 19870626
Record Date Completed: 19870626

2/9/10 (Item 10 from file: 155)
DIALOG(R) File 155:MEDLINE(R)
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06715270 PMID: 6440948

Complementation analysis of the aliphatic amidase genes of *Pseudomonas aeruginosa*.

Drew R

Journal of general microbiology (ENGLAND) Dec 1984, 130 (Pt 12)
p3101-11, ISSN 0022-1287 Journal Code: 0375371

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

A plasmid, pCL34, capable of autonomous replication in *Escherichia coli* and *Pseudomonas aeruginosa* has been constructed which carries the promoter and structural gene (*amiE*) for *P. aeruginosa* amidase, but not the regulator gene (*amiR*). Plasmid pCL34 has been mobilized from *E. coli* to *P. aeruginosa* using the broad host range plasmid RP4. Complementation studies were performed in *P. aeruginosa* strains carrying various amidase mutations. Measurements of amidase activity in the recipients under inducing, non-inducing and repressing conditions showed trans-complementation by the chromosomally located regulator gene product. These results confirmed the positive control model for amidase gene expression. Levels of amidase expression seen during these studies were approximately threefold higher than in the parental, amidase-positive strains.

Tags: Support, Non-U.S. Gov't

Descriptors: *Amidohydrolases--genetics--GE; *Genes, Bacterial; *Genes, Structural; **Pseudomonas aeruginosa*--genetics--GE; Chromosome Mapping; Gene Expression Regulation; Genetic Complementation Test; Phenotype; Plasmids; *Pseudomonas aeruginosa*--enzymology--EN; Transformation, Bacterial

CAS Registry No.: 0 (Plasmids)

Enzyme No.: EC 3.5. (Amidohydrolases)

Record Date Created: 19850314

Record Date Completed: 19850314

2/9/11 (Item 11 from file: 155)
DIALOG(R) File 155:MEDLINE(R)
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05674138 PMID: 6793036

Chloroacetone as an active-site-directed inhibitor of the aliphatic amidase from *Pseudomonas aeruginosa*.

Hollaway M R; Clarke P H; Ticho T

Biochemical journal (ENGLAND) Dec 1 1980, 191 (3) p811-26, ISSN 0264-6021 Journal Code: 2984726R

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

1. Chloroacetone (I) was shown to be an active-site-directed inhibitor of the aliphatic amidase (EC 3.5.1.4) from *Pseudomonas aeruginosa* strain PAC142.2. This inhibitor reacted with the enzyme in two stages: the first involving the reversible formation of an enzymically inactive species, EI, and the second the formation of a species, EX, from which enzymic activity could not be recovered. 3. Different types of kinetic experiment were conducted to test conformity of the reaction to the scheme: $E + I \xrightleftharpoons{k+1} EI \xrightarrow{k-1} E + I$ Leads to $E + I \xrightleftharpoons{k+2} EX \xrightarrow{k-2} E + I$ A computer-based analysis of the results was carried out and values of the individual rate constants were determined. 4. No direct evidence for a binding step before the formation of EI could be obtained, as with $[E]_0$ Less Than $[I]_0$ the observed first-order rate constant for the formation of EI was directly proportional

to the concentration of chloroacetone up to 1.2 mM (above this concentration the reaction became too rapid to follow even by the stopped-flow method developed to investigate fast inhibition). 5. The value of k_{+1} exhibited a bell-shaped pH-dependency with a maximum value of about $3 \times 10(3) \text{ M}^{-1} \text{ S}^{-1}$ at pH6 and apparent pK_a values of 7.8 and about 4.8.6. The values of k_{-1} and K_{+2} were similar and changed with the time of reaction from values of about $3 \times 10(-3) \text{ S}^{-1}$ (pH8.6) at short times to about one-sixth this value for longer periods of incubation. In this respect the simple reaction scheme is insufficient to describe the inhibition process. 7. The overall inhibition reaction is rapid, whether it is considered in relation to the expected chemical reactivity of chloroacetone, the rate of reaction of other enzymes with substrate analogues containing the chloromethyl group, or the rate of the amidase-catalysed hydrolysis of N-methylacetamide, a substrate that is nearly isosteric with chloroacetone. 8. Acetamide protected the amidase from inhibition by chloroacetone, and the concentration-dependence of the protection gave a value of an apparent dissociation constant similar to the K_m value for this substrate. 9. Addition of acetamide to solutions of the species EI led to a slow recovery of activity. Recovery of active enzyme was also observed after dilution of a solution of EI in the absence of substrate. 10. The species EI is considered not to be a simple adsorption complex, and the possibilities are discussed that it may be a tetrahedral carbonyl adduct, a Schiff base (azomethine) or a complex in which the enzyme has undergone a structural change. The species EX is probably a derivative in which there is a covalent bond between a group in the enzyme and the C-1 atom of the inhibitor.

Descriptors: *Acetone--analogs and derivatives--AA; *Amidohydrolases--antagonists and inhibitors--AI; *Pseudomonas aeruginosa--enzymology--EN; Acetamides--pharmacology--PD; Acetone--pharmacology--PD; Binding Sites; Kinetics; Models, Chemical

CAS Registry No.: 0 (Acetamides); 67-64-1 (Acetone); 78-95-5 (chloroacetone)

Enzyme No.: EC 3.5. (Amidohydrolases); EC 3.5.1.4 (amidase)

Record Date Created: 19811119

Record Date Completed: 19811119

2/9/13 (Item 13 from file: 155)

DIALOG(R) File 155:MEDLINE(R)

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05067535 PMID: 110589

Inhibition of the aliphatic amidase from Pseudomonas aeruginosa by urea and related compounds.

Gregoriou M; Brown P R

European journal of biochemistry / FEBS (GERMANY, WEST) May 2 1979, 96

(1) p101-8, ISSN 0014-2956 Journal Code: 0107600

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

The time-dependent inhibition of amidase from Pseudomonas aeruginosa strain AI 3 by urea, hydroxyurea and cyanate displayed saturation kinetics fitting a model for the reaction sequence in which formation of a complex in a reversible step was followed by an irreversible step. Altered amidases from mutant strains AIU 1N and OUCH 4, selected for their resistance to inhibition of growth by urea and hydroxyurea respectively, had altered kinetic constants for inhibition indicating reduced binding capacity for the inhibitors. The substrate acetamide protected AI 3 amidase against inhibition by urea, and altered K_i values for inhibition of the mutant amidases were paralleled by alterations in K_m values for acetamide indicating that urea acted at the active site. Inhibition of AI 3 amidase involved the binding of one molecule of urea per molecule of enzyme. Urea inhibited amidase slowly regained activity at pH 7.2 through release of urea.

Descriptors: *Amidohydrolases--antagonists and inhibitors--AI; *Pseudomonas aeruginosa--enzymology--EN; *Urea--pharmacology--PD; Cyanates--pharmacology--PD; Enzyme Activation; Hydroxyurea--pharmacology--PD;

Kinetics; Molecular Weight

CAS Registry No.: 0 (Cyanates); 127-07-1 (Hydroxyurea); 57-13-6 (Urea)

Enzyme No.: EC 3.5. (Amidohydrolases)

Record Date Created: 19790925

Record Date Completed: 19790925

2/9/14 (Item 14 from file: 155)

DIALOG(R) File 155:MEDLINE(R)

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05063754 PMID: 110350

Kinetic mechanism of the aliphatic amidase from *Pseudomonas aeruginosa*.

Woods M J; Findlater J D; Orsi B A

Biochimica et biophysica acta (NETHERLANDS) Mar 16 1979, 567 (1) p225-37, ISSN 0006-3002 Journal Code: 0217513

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

The kinetic constants for hydrolysis and transfer (with hydroxylamine as the alternate acceptor) of the aliphatic amidase (acylamide amidohydrolase, EC 3.5.1.4) from *Pseudomonas aeruginosa* were determined for a variety of acetyl and propionyl derivatives. The results obtained were consistent with a ping-pong or substitution mechanism. Product inhibition, which was pH dependent, implicated an acyl-enzyme compound as a compulsory intermediate and indicated that ammonia combined additionally with the free enzyme in a dead-end manner. The uncompetitive activation of acetamide hydrolysis by hydroxylamine and the observation that the partitioning of products between acetic acid and acetohydroxamate was linearly dependent on the hydroxylamine concentration substantiated these conclusions and indicated that deacylation was at least partially rate limiting. With propionamide as the acyl donor apparently anomalous results, which included inequalities in certain kinetic constants and a hyperbolic dependence of the partition ratio on the hydroxylamine concentration, could be explained by postulating a compulsory isomerisation of the acyl-enzyme intermediate prior to the transfer reaction.

Descriptors: *Amidohydrolases--metabolism--ME; **Pseudomonas aeruginosa*--enzymology--EN; Acetamides; Acetic Acids--pharmacology--PD; Acylation; Amides; Amidohydrolases--antagonists and inhibitors--AI; Binding Sites; Hydrolysis; Hydroxylamines--pharmacology--PD; Kinetics; Models, Chemical; Propionates

CAS Registry No.: 0 (Acetamides); 0 (Acetic Acids); 0 (Amides); 0 (Hydroxylamines); 0 (Propionates)

Enzyme No.: EC 3.5. (Amidohydrolases)

Record Date Created: 19790925

Record Date Completed: 19790925

2/9/16 (Item 16 from file: 155)

DIALOG(R) File 155:MEDLINE(R)

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04287097 PMID: 932686

Regulatory properties of an inducible aliphatic amidase in a thermophilic bacillus.

Thalenfeld B; Grossowicz N

Journal of general microbiology (ENGLAND) May 1976, 94 (1) p131-41, ISSN 0022-1287 Journal Code: 0375371

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

A thermophilic bacillus growing on acetamide as both carbon and nitrogen sources produces an inducible amidase. This amidase hydrolysed the

following amides in decreasing order of activity, in comparison with acetamide (1.00): propionamide (0.97), fluoroacetamide (0.84), formamide (0.35) and glycineamide (0.12). Cyanoacetamide, dimethylacetamide, dimethylformamide and urea also induced the synthesis of the amidase, but were not substrates of the enzyme. Studies with protoplasts suggest that the amidase is located in the cytoplasm. Glucose strongly inhibited amidase synthesis; and limiting nitrogen did not release this inhibition. Urea strongly inhibited amidase activity in a competitive manner; but the inhibition caused by iodoacetamide and cyanoacetamide was non-competitive. Both thioacetamide and thiourea were effective inhibitors of enzyme induction. Bacteria grown on a succinate-minimal medium exhibited a lag in amidase synthesis, which could be eliminated by decreasing the concentration of succinate. Acetate- or pyruvate-grown cultures behaved similarly, while those grown on alanine or glutamate exhibited no lag in enzyme induction. In the mutant strain E21, repression of amidase synthesis by glucose was much less evident and no lag for induction was apparent with any of the other carbon sources mentioned.

Descriptors: *Amidohydrolases--biosynthesis--BI; *Bacillus--enzymology--EN; Acetamides--metabolism--ME; Amides--metabolism--ME; Amidohydrolases--metabolism--ME; Bacillus--growth and development--GD; Bacillus--metabolism--ME; Cell-Free System; Cytoplasm--enzymology--EN; Enzyme Induction--drug effects--DE; Enzyme Repression; Glucose--pharmacology--PD; Heat; Kinetics; Protoplasts--enzymology--EN; Thioacetamide--pharmacology--PD; Thiourea--pharmacology--PD; Urea--pharmacology--PD

CAS Registry No.: 0 (Acetamides); 0 (Amides); 50-99-7 (Glucose); 57-13-6 (Urea); 62-55-5 (Thioacetamide); 62-56-6 (Thiourea)

Enzyme No.: EC 3.5. (Amidohydrolases)

Record Date Created: 19760823

Record Date Completed: 19760823

2/9/19 (Item 19 from file: 155)

DIALOG(R) File 155:MEDLINE(R)

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03398192 PMID: 4625925

Biochemical and immunological comparison of aliphatic amidases produced by Pseudomonas species.

Clarke P H

Journal of general microbiology (ENGLAND) Jul 1972, 71 (2) p241-57,

ISSN 0022-1287 Journal Code: 0375371

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

Descriptors: *Amidohydrolases--biosynthesis--BI; *Pseudomonas--enzymology--EN; Acetamides--metabolism--ME; Antigens; Cell-Free System; Cross Reactions; Culture Media; Electrophoresis, Starch Gel; Enzyme Induction; Formamides--metabolism--ME; Genes, Regulator; Genes, Structural; Hydrolases--analysis--AN; Hydrolysis; Immune Sera; Immunodiffusion; Mutation; Phenotype; Pseudomonas--metabolism--ME; Pseudomonas aeruginosa--enzymology--EN; Pseudomonas aeruginosa--immunology--IM; Transferases--analysis--AN

CAS Registry No.: 0 (Acetamides); 0 (Antigens); 0 (Culture Media); 0 (Formamides); 0 (Immune Sera)

Enzyme No.: EC 2. (Transferases); EC 3. (Hydrolases); EC 3.5. (Amidohydrolases)

Record Date Created: 19720922

Record Date Completed: 19720922

2/9/22 (Item 2 from file: 5)

DIALOG(R) File 5: Biosis Previews(R)

(c) 2004 BIOSIS. All rts. reserv.

0011231256 BIOSIS NO.: 199800025503

The aliphatic amidase : Another way to produce ammonia in H. pylori?

AUTHOR: Skouloubris S; Labigne A; De Reuse H

AUTHOR ADDRESS: Inst. Pasteur, Paris, France**France

JOURNAL: Gut 41 (SUPPL. 1): pA14 1997 1997
MEDIUM: print
CONFERENCE/MEETING: European Helicobacter Pylori Study Group Xth
International Workshop on Gastroduodenal Pathology and Helicobacter Pylori
Lisbon, Portugal September 11-14, 1997; 19970911
SPONSOR: European Helicobacter pylori Study Group
ISSN: 0017-5749
DOCUMENT TYPE: Meeting; Meeting Abstract
RECORD TYPE: Citation
LANGUAGE: English
REGISTRY NUMBERS: 7664-41-7: ammonia
DESCRIPTORS:

MAJOR CONCEPTS: Enzymology--Biochemistry and Molecular Biophysics;
Molecular Genetics--Biochemistry and Molecular Biophysics
BIOSYSTEMATIC NAMES: Aerobic Helical or Vibrioid Gram-Negatives--
Eubacteria, Bacteria, Microorganisms
ORGANISMS: Helicobacter-pylori (Aerobic Helical or Vibrioid
Gram-Negatives)
COMMON TAXONOMIC TERMS: Bacteria; Eubacteria; Microorganisms
CHEMICALS & BIOCHEMICALS: aliphatic amidase; ammonia--metabolic
production pathways
MISCELLANEOUS TERMS: Meeting Abstract; Meeting Abstract
CONCEPT CODES:
31500 Genetics of bacteria and viruses
10050 Biochemistry methods - General
10054 Biochemistry methods - Proteins, peptides and amino acids
10808 Enzymes - Physiological studies
13002 Metabolism - General metabolism and metabolic pathways
13012 Metabolism - Proteins, peptides and amino acids
31000 Physiology and biochemistry of bacteria
00520 General biology - Symposia, transactions and proceedings
10060 Biochemistry studies - General
10064 Biochemistry studies - Proteins, peptides and amino acids
36002 Medical and clinical microbiology - Bacteriology
BIOSYSTEMATIC CODES:
06210 Aerobic Helical or Vibrioid Gram-Negatives

2/9/45 (Item 1 from file: 65)
DIALOG(R) File 65: Inside Conferences
(c) 2004 BLDSC all rts. reserv. All rts. reserv.

03333046 INSIDE CONFERENCE ITEM ID: CN035225547

Identification of an aliphatic amidase in H. pylori

de Reuse, H.; Skouloubris, S.; Labigne, A.

CONFERENCE: Campylobacter, heliobacter & related organisms-
International workshop; 9th
P: 490

Institute of Child Health, 1998

ISBN: 0620216794

LANGUAGE: English DOCUMENT TYPE: Conference Papers

CONFERENCE EDITOR(S): Lastovica, A. J.; Newell, D. G.; Lastovica, E. E.

CONFERENCE SPONSOR: University of Cape Town

CONFERENCE LOCATION: Cape Town

CONFERENCE DATE: Sep 1997 (199709) (199709)

BRITISH LIBRARY ITEM LOCATION: m00/31914

DESCRIPTORS: campylobacter; heliobacter; organisms; child health

?t s2/3,kwic/36 37 39 40 41 43 44 48

>>>KWIC option is not available in file(s): 399

2/3,KWIC/36 (Item 2 from file: 357)
DIALOG(R) File 357: Derwent Biotech Res.
(c) 2004 Thomson Derwent & ISI. All rts. reserv.

0230013 DBR Accession No.: 99-00114 PATENT

**New Helicobacter sp. aliphatic amidase AmiE polypeptides and their
encoding sequence - Helicobacter pylori recombinant protein
preparation, vector expression in host cell and DNA probe and**

monoclonal antibody, used for infection diagnosis, recombinant vaccine or therapy

AUTHOR: de Reuse H; Skouloubris S; Labigne A
CORPORATE SOURCE: Paris, France.
PATENT ASSIGNEE: Inst.Pasteur-Paris; INSERM 1998
PATENT NUMBER: WO 9844094 PATENT DATE: 981008 WPI ACCESSION NO.:
98-557106 (9847)
PRIORITY APPLIC. NO.: US 41745 APPLIC. DATE: 970328
NATIONAL APPLIC. NO.: WO 98EP1824 APPLIC. DATE: 980327
LANGUAGE: English

New Helicobacter sp. aliphatic amidase AmiE polypeptides and their encoding sequence

2/3,KWIC/37 (Item 3 from file: 357)
DIALOG(R)File 357:Derwent Biotech Res.
(c) 2004 Thomson Derwent & ISI. All rts. reserv.

0203740 DBR Accession No.: 96-14511
Utilization of acetonitrile and other aliphatic nitriles by a Candida famata strain - acetonitrile degradation using nitrile-hydratase and amidase activity
AUTHOR: Linardi V R; Dias J C T; Rosa C A
CORPORATE AFFILIATE: Univ.Minas-Gerais-Fed.Inst.Biol.Sci.
CORPORATE SOURCE: Departamento de Microbiologia, Instituto de Ciencias Biologicas, Universidade Federal de Minas Gerais, C.P. 486, Belo Horizonte, MG 31270-901, Brazil.
JOURNAL: FEMS Microbiol.Lett. (144, 1, 67-71) 1996
ISSN: 0378-1097 CODEN: FMLED7
LANGUAGE: English

Utilization of acetonitrile and other aliphatic nitriles by a Candida famata strain - acetonitrile degradation using nitrile-hydratase and amidase activity

2/3,KWIC/39 (Item 1 from file: 340)
DIALOG(R)File 340:CLAIMS(R)/US Patent
(c) 2004 IFI/CLAIMS(R). All rts. reserv.

3528971 0122998
C/HELICOBACTER ALIPHATIC AMIDASE AMIE POLYPEPTIDES, AND DNA SEQUENCES ENCODING THOSE POLYPEPTIDES; SCREENING BY CONTACTING ENZYME WITH COMPOUND, AND SELECTING COMPOUND WHICH INHIBITS ENZYME ACTIVITY; ANTIULCER AGENTS; BACTERICIDES
Inventors: De Reuse Hilde (FR); Labigne Agnes (FR); Skouloubris Stephane (FR)
Assignee: Institut Pasteur FR
Assignee Code: 42312

	Kind	Publication Number	Date	Application Number	Date
	B	US 6248551	20010619	US 9827900	19980223
Priority Applic:				US 9827900	19980223
Provisional Applic:				US 60-41745	19970328
Calculated Expiration:					20180223

HELICOBACTER ALIPHATIC AMIDASE AMIE POLYPEPTIDES, AND DNA SEQUENCES ENCODING THOSE POLYPEPTIDES...

2/3,KWIC/40 (Item 2 from file: 340)
DIALOG(R)File 340:CLAIMS(R)/US Patent
(c) 2004 IFI/CLAIMS(R). All rts. reserv.

3168988 9921350
C/PREPARATION OF LACTAMS FROM ALIPHATIC ALPHA, OMEGA-DINITILES; ISOLATED

COMAMONAS TESTOSTERONI 5-MGAM-4D WITH NITRILE HYDRATASE AND AMIDASE ACTIVITIES; FOR HIGH YIELD WITH HIGH REGIOSELECTIVITY AND BY PRODUCT INHIBITION

Inventors: Di Cosimo Robert (US); Fallon Robert Donald (US); Gavagan John Edward (US); Herkes Frank Edward (US)
Assignee: Du Pont de Nemours, E I & Co
Assignee Code: 25048

	Kind	Publication Number	Date	Application Number	Date
	A	US 5922589	19990713	US 98108729	19980701
Division of:		US 5858736		US 96650073	19960517
Priority Applic:				US 98108729	19980701
				US 96650073	19960517

Calculated Expiration: 20160517

**PREPARATION OF LACTAMS FROM ALIPHATIC ALPHA, OMEGA-DINITILES...
...ISOLATED COMAMONAS TESTOSTERONI 5-MGAM-4D WITH NITRILE HYDRATASE AND AMIDASE ACTIVITIES; FOR HIGH YIELD WITH HIGH REGIOSELECTIVITY AND BY PRODUCT INHIBITION**

2/3,KWIC/41 (Item 3 from file: 340)
DIALOG(R) File 340:CLAIMS(R)/US Patent
(c) 2004 IFI/CLAIMS(R). All rts. reserv.

3096789 9901716

**C/PREPARATION OF LACTAMS FROM ALIPHATIC ALPHA, OMEGA-DINITRILES;
CONTACTING DINITRILE IN AQUEOUS MIXTURE WITH ENZYME CATALYST HAVING ALIPHATIC NITRILASE ACTIVITY OR COMBINATION OF NITRILE HYDRATASE AND AMIDASE ACTIVITY, CONTACTING PRODUCT WITH HYDROGEN AND HYDROGENATION CATALYST TO PRODUCE LACTAM**

Inventors: Di Cosimo Robert (US); Fallon Robert Donald (US); Gavagan John Edward (US); Herkes Frank Edward (US)
Assignee: Du Pont de Nemours, E I & Co
Assignee Code: 25048

	Kind	Publication Number	Date	Application Number	Date
	A	US 5858736	19990112	US 96650073	19960517
Priority Applic:				US 96650073	19960517

Calculated Expiration: 20160517
CERTIFICATE OF CORRECTION: 19990928

**PREPARATION OF LACTAMS FROM ALIPHATIC ALPHA, OMEGA-DINITRILES...
...CONTACTING DINITRILE IN AQUEOUS MIXTURE WITH ENZYME CATALYST HAVING ALIPHATIC NITRILASE ACTIVITY OR COMBINATION OF NITRILE HYDRATASE AND AMIDASE ACTIVITY, CONTACTING PRODUCT WITH HYDROGEN AND HYDROGENATION CATALYST TO PRODUCE LACTAM**

2/3,KWIC/43 (Item 2 from file: 654)
DIALOG(R) File 654:US Pat.Full.
(c) Format only 2004 The Dialog Corp. All rts. reserv.

4166734

Derwent Accession: 1998-041747

Utility

**C/ Preparation of lactams from aliphatic [alpha],[omega]-Dinitiles
; ISOLATED COMAMONAS TESTOSTERONI 5-MGAM-4D WITH NITRILE HYDRATASE AND AMIDASE ACTIVITIES; FOR HIGH YIELD WITH HIGH REGIOSELECTIVITY AND BY PRODUCT INHIBITION**

Inventor: Di Cosimo, Robert, Rockland, DE
Fallon, Robert Donald, Elkton, MD
Gavagan, John Edward, Wilmington, DE

Herkes, Frank Edward, Wilmington, DE
Assignee: E. I. du Pont de Nemours and Company (02), Wilmington, DE
Du Pont de Nemours, E I & Co (Code: 25048)
Examiner: Lilling, Herbert J. (Art Unit: 161)

	Publication Number	Kind	Date	Application Number	Filing Date
Main Patent	US 5922589	A	19990713	US 98108729	19980701
Division	US 5858736	A	19990112	US 96650073	19960517

Fulltext Word Count: 19383

Preparation of lactams from aliphatic [alpha],[omega]-Dinitiles

2/3,KWIC/44 (Item 3 from file: 654)
DIALOG(R)File 654:US Pat.Full.
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4095232
Derwent Accession: 1998-041747

Utility

CERTIFICATE OF CORRECTION

C/ Preparation of lactams from aliphatic [alpha],[omega]-dinitriles
; CONTACTIN G DINITRILE IN AQUEOUS MIXTURE WITH ENZYME CATALYST HAVING
ALIPHATIC NITRILASE ACTIVITY OR COMBINATION OF NITRILE HYDRATASE AND
AMIDASE ACTIVITY, CONTACTING PRODUCT WITH HYDROGEN AND HYDROGENATION
CATALYST TO PRODUCE LACTAM

Inventor: Di Cosimo, Robert, Rockland, DE
Fallon, Robert Donald, Elkton, MD
Gavagan, John Edward, Wilmington, DE
Herkes, Frank Edward, Wilmington, DE

Assignee: E. I. du Pont de Nemours and Company (02), Wilmington, DE
Du Pont de Nemours, E I & Co (Code: 25048)

Examiner: Lilling, Herbert J. (Art Unit: 161)

	Publication Number	Kind	Date	Application Number	Filing Date
Main Patent	US 5858736	A	19990112	US 96650073	19960517

Fulltext Word Count: 20552

Preparation of lactams from aliphatic [alpha],[omega]-dinitriles

2/3,KWIC/48 (Item 1 from file: 349)
DIALOG(R)File 349:PCT FULLTEXT
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00453630
**i(HELICOBACTER) ALIPHATIC AMIDASE POLYPEPTIDES, DNA SEQUENCES ENCODING
THOSE POLYPEPTIDES AND USES THEREOF**
**POLYPEPTIDES DE L' AMIDASE ALIPHATIQUE Amie D'i(HELICOBACTER)ET SEQUENCES
D'ADN CODANT LESDITS POLYPEPTIDES**

Patent Applicant/Assignee:

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Patent and Priority Information (Country, Number, Date):

Patent: WO 9844094 A2 19981008

Application: WO 98EP1824 19980327 (PCT/WO EP9801824)
Priority Application: US 9741745 19970328
Designated States: AL AM AT AU AZ BA BB BG BR BY CA CH CN CU CZ DE DK EE ES
FI GB GE GH GM GW HU IL IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MD MG
MK MN MW MX NO NZ PL PT RO RU SD SE SG SI SK SL TJ TM TR TT UA UG US UZ
VN YU ZW GH GM KE LS MW SD SZ UG ZW AM AZ BY KG KZ MD RU TJ TM AT BE CH
DE DK ES FI FR GB GR IE IT LU MC NL PT SE BF BJ CF CG CI CM GA GN ML MR
NE SN TD TG
Publication Language: English
Fulltext Word Count: 9017

i(HELICOBACTER) ALIPHATIC AMIDASE POLYPEPTIDES, DNA SEQUENCES ENCODING
THOSE POLYPEPTIDES AND USES THEREOF
POLYPEPTIDES DE L' AMIDASE ALIPHATIQUE Amie D'i(HELICOBACTER) ET SEQUENCES
D'ADN CODANT LESDITS POLYPEPTIDES
?logoff hold

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\$22.06 Estimated cost this search
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Search Results - Record(s) 1 through 4 of 4 returned.

L7: Entry 1 of 4

File: PGPB

Sep 25, 2003

PGPUB-DOCUMENT-NUMBER: 20030180330
DOCUMENT-IDENTIFIER: US 20030180330 A1

TITLE: Method for identifying helicobacter antigens
PUBLICATION-DATE: September 25, 2003

US-CL-CURRENT: 424/234.1; 435/7.32, 530/350
INT-CL: [07] G01 N 33/554, G01 N 33/569, A61 K 39/02, C07 K 14/195

L7: Entry 2 of 4

File: USPT

Jun 19, 2001

US-PAT-NO: 6248551
DOCUMENT-IDENTIFIER: US 6248551 B1

TITLE: Helicobacter aliphatic amidase AmiE polypeptides, and DNA sequences encoding those polypeptides

DATE-ISSUED: June 19, 2001

US-CL-CURRENT: 435/18; 435/106, 435/228, 435/32, 435/6, 514/2, 530/344, 530/350INT-CL: [07] A61 K 39/02

L7: Entry 3 of 4

File: DWPI

Sep 25, 2003

DERWENT-ACC-NO: 2001-639461
ABSTRACTED-PUB-NO: WO 200183531A
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TITLE: Helicobacter proteins, used for producing vaccines against H. pylori infection, and related gastritis, cancers and ulcers

INT-CL (IPC): A61 K 39/02, C07 K 14/195, C07 K 14/205, G01 N 33/38, G01 N 33/554,
G01 N 33/569

Derwent-CL (DC): B04, D16 , S03

CPI Codes: B04-B04C1; B14-A01; B14-E08; B14-E10B; B14-H01; B14-H01B; B14-S11B; B14-S11C; D05-H07; D05-H13;

EPI Codes: S03-E14D1; S03-E14D4; S03-E14H4;

L7: Entry 4 of 4

File: DWPI

Oct 8, 1998

DERWENT-ACC-NO: 1998-557106
ABSTRACTED-PUB-NO: US 6248551B
COPYRIGHT 2004 DERWENT INFORMATION LTD

TITLE: New Helicobacter aliphatic amidase AmiE polypeptides and their encoding sequences - used in diagnosis, treatment and prevention of Helicobacter sp. infections in humans and animals

- INT-CL (IPC): A61 K 39/02, C12 N 9/00

Derwent-CL (DC): B04, C06 , D16

CPI Codes: B04-C01; C04-C01; B04-E02E; C04-E02E; B04-E08; C04-E08; B04-F0100E; C04-F0100E; B04-G21; C04-G21; B04-L05; C04-L05; B04-N03; C04-N03; B12-K04; C12-K04; B14-E08; C14-E08; D05-H12B2; D05-H14; D05-H17; D05-H17A3; D05-H19;

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